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C.Species Neston sp.
A.Noter Nostons sp. strain PCC 7120 is a synonym of Anabaona sp. strain PCC 7120
C.Forton 14 (Nove-2001) secquence_revision 14 (Nove-2001) strain_change 30.500.2003
C.Socession: AE2341
S.Sockon, T., Rokanura, Y., Wolk, C.P., Kuritz, T., Sasamoto, S., Matanabe, A., Iriquehi
Nakazaki, N., Shimpe, S., Sugimete, M., Pakazawi, M., Yamada, M., Yasuda, M., Talata, S.
G. K., Okumura, S., Shimpo, S., Takeuchi, C.; Wada, I.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Syncobocystis
                                                                                                                                                                                                                                                                                                 A,Molecule type. DNA
A,Residues. 1-490 «KAN»
A,Cross-references: EMRI-D40914; GR ABOR1213, NTD 91/53477, PIEN-BAA18428.1; PIEL-d101916
A,Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
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A)Accession: AE2341
A)Accession: AE2341
A)Actuar: preliminary
A)Molecule type: DNA
A)Residues: 1-497 < KUD>
A)Residues: 1-497 < KUD>
A)Residues: 1-497 < KUD>
C)COBETION OF COBETION OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 14.0%; Score 395; DB 2; Length 490; Best Leval Similaring 28.0%; Pred Nr. 2.10.20; Matches 144; Conservative 75; Mismatches 211; Indels 84; Gaps
                                                                                                                                                                         A; Reference number: S74322; MUID: 97061201; PMID, 8905231
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                                                                                                                                                                                                                 A;Accession: S76169
A;Status: preliminary
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A; Gene: al14284

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A,Title, Cloudny of a wilt responsive cDNA from an Arabidopsis thaliana suspension on A;Reference number, 224454
A;Reference number, 224454
A;Accession: T51734
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                                                                                                                                                                                                                                                                                                 79 YNCNIEANEIV-VSEFGIMAYPUPCKNIFAKAFSYLSHIIPEFIUWJLINIMETGDDYYA 137
                                                                                                                                                                                                                                                                                                                                                                        99. YLAEKNAGKILHPGVFGTQKPGGWLANIFDFKLKNIANT-------NVIYWGEKLLA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148 TWEAAPPHREDPKTEDTLOKEYPHOVESAGEAFGAHPPFEDSCEQONGAPCT VNESTKIG 207
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                                                                                                                                                    19 EVÇEÇLETMIÇEVLI PINSPGMHTIGITKYNHWERGI ALI HSETTEKIGEVYYEKKELKSDI (78
                                                                                                                                                                                            38 DVEGELPIELGGLEERNSPGILLIKGGETHPFELGGGMENTSFYWGFARYPNSFVKTEG 97
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                                                                              Indels 83;
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Length 497;
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25.6%; Pred. No. 4.5e-19;
iive 93; Mismatches 211;
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A,Residues: 1-538 <NEI>
A,Cross-references: EMBL:AJUU5813; PIDN:CAAU6712.1
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                                                                          Matches 133; Conservative
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235 KHIEVVCSIPSESLLAFSYRHSFOITENTIVITEOPEKLDIVKLATATIFGYNARS' 272 1	DNA Res 3, 104-136, 1946 A)Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys s. A) Recession: \$76206 A) Recession: \$76206 A) Section: preliminary A) Molecule type: DNA A, Residues: preliminary A, Molecule type: DNA A, Residues: Preliminary A, Molecule type: DNA A, Residues: EMBL:D90914; GB:AB001349; NID:q1654477; PIDN:BAA18465.1; PID:d101 A, Cross references: EMBL:D90914; GB:AB001349; NID:q1654477; PIDN:BAA18465.1; PID:d101 A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1946 Query Match A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1946 A; Note: Local Similarity 23 4%; Prod HA 2 20-12; Matches 113; Conservative 90; Mismatches 210; Indels 70; Sups 19; Matches 113; Conservative 90; Mismatches 210; Indels 70; Sups 19; A) B) FINENKEEHPEPIKAEVOGQLPTWIOGVILRNGPGMHFIGDTKYNHWFDGIALHSFTFKN 64 H FS:MAVEFLFTSLITISSQ1FAETHSSTSFRSSHYGHWFDGIALHAVHGE 73 H FS:MAVEFLFTSLITISSQ1FAETHSSTSFRSSHYGHWFDGIALAVHGE 73	CA CANADA CONTRACT CANAD
123 NCLINI	manus: protein MAA21.150 abidopsis thallana (mouse-ear cress) abidopsis thallana (mouse-ear cress) 10.2000 #sequence_revision ob-thn-ranger manueller-Auer, S.; Zipp, M.; Schaefer, N. Mueller-Auer, S.; Zipp, M.; Schaefer, N. Mueller-Sequence Database, April 200 minery per DNA 5.8 ePFs 6.8 e	Output Match

Db 414 VEDGGMLIT-YVVFTGEESSFIVVINAGGINSFPTARVITPQEVDYGFHGIWVIEEQL 470 PESULT 10 T07123 In the cis-epoxycarotenoid dioxygenase - tomato N,Alburda-t names privabile measurethin diaxygenase - tomato C; bate: 30-Apr-1999 #sequence_revision 30 Apr 1999 #text_change 20-Jun-2000 C; bate: 40-Apr-1999 #sequence_revision 30 Apr 1999 #text_change 20-Jun-2000 R; Burbhidge, A. submitted to the EMBL Data Library, January 1998	A; Reference number: 215934 A; Reference number: 215934 A; Accession: T07123 A; Status: preliminary: translated from GB/EMBL/DDBJ A; Molecule type: mRNA A; Resillates: £.665 .E3F A; Cross-references: EMBL; 797215; piDN:CAB10168.1 Querty Match Best Local Similarity 23.4%; Prof. No. 8.6e-12; Matches 133, Conservative 97, Mismatches 219; Indets 120; Gaps 28; QY I METIFURNKEEHPEPIRAE	27	\$19. VEDIVAYENSEYLERIJERIJERIJERIJERIJERIJERIJERIJERIJERIJ	RESULT 11 Tables
Oy 361 PLOYDKTAFVGSNIJVKI PISALAVERLGSIYGQPEILGEGJELPHVNIJYNGKKYKYVY 420 327 AVKTSTDGQLMQATIAN-PQTAKIVELINVLSPSGEPRYTNPOPTGQDWPYTY 377 OY 421ATEVQMSPVPTKIAKLNVQTKEV- LHWGEDHCWPSIPTEVPSPAREEDEGVVL 473 Db 378 MALQPPAEILGSQWFGEJAPTEYHTGLVIJAKLGE-HQYFVLFLXIPHELLGGCGM11 434 OY 474 TCV 476 Db 435 TVV 437	RESULT 9 Ag1944 hypothetical protein alliant [inported] Tanker sp. (strain PCC 7128) C.Species: Nostoc sp. Anote: Nostoc sp. Strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C.Date: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C.Date: Nostoc sp. C.Date	Query Match Bost Local Similarity 21.7%: Prod. No. 3.7c.12; Matches 117; Conservative 95; Mismatehes 224; Indels 107; Saps 23; Qy 3 IIENPAREEHPEPIKAEVO	OY 113 ESHTIPEFTUNCLINIMKIGDDYYALSEINFIPMIGDALEHTEKVIYSKYVANNTAISH 172 125 TGNTALIWHAGGLALWEGGAPY	Oy 352 IPTCKREVVPLQYDRDAEVGSNLVKLPTSATAVKEKINGSIYCQPELLCE-GIELPPVVVD 410 12.

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Apdrossiteterendes (GRPBR) (GRPB) PHAN-BAR76594.1; PID:q17134033; GSPDB:GN00179
Apstrontontal source: strain PCC 7120
                                                                 A; Molecule type: DNA
A; Residues: 1.472 <KUR>
                                         A;Status: preliminary
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      A; Accession: AG2417
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Nakazaki, N.; Shimpo, S.; Suqimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
INA Res. 8, 205-213, 2001
A. Hille: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A; Reference number: AB1807; Muid:21595285; PMID:11759840
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                                                                                                                                                                                                                                                                                                                                                                                        Query Match 9.5%; Score 269; DB 2; Length 790;
Best Local Similarity 22.6%; Pred. No. 4e-11;
Matches 136; Conservative 91; Mismatches 221; Indels 154; Gaps 28;
                                                                                             A;Wolecule type: DNA
A;Festlars 1 70 AUL.
A;Coss-references: EMH-H53341; PIDN:AACK9106 1: GSPDR-GN00028; CFSP-F49E10 2
A;Experimental source: strain Bristol N2; clone F49E10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----QIKEVLHWGEDHCWPSEPIFVP 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               441 FPYQWGYIVQHPFAS-CNSITKINVDEPAGNBNLEFPAEPTLVLH------FPWFVQ 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79 ALGAVGSFHVSNGQVVFSAQYYPAPPYKIWEFYDRNMSKASVPWAGWSDYNLTAMSRWEO 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96 M-AYPDPCKNIFAKAFSYLSHTIPEFTDNCLINIMKTGDDYYATSETNFI--RKIDPQTL, 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139 VPANPDSAR------FHPN--LDFWKVGNRIVAGTEAPYWVGYEFDVRTL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          153 ETLDKVDYSK-----MGTSI 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 OKFKLFPFKEENDIFSTPRHTMIPISMAI-HERNDADGTIWGSFSAMNFEEQRFFQGIFT 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 VDKGRTKYVLFKIPSSVPEKEKKKSCFKHLEVVCSIPSRSLLQPSYYHSFGITENYIV-- 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 -----FIEOPFKI.DIVKLATAYIRGVNWASCI.SFHKEDKTWFHFVDRKTKKEVST 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    293 ITSLLINPCKFKEPPLN----NVRSAIQKGGLWG--MDFYDMVPMRFLIFNKKTLEFTTS 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              297 K--FYTDALVLYHHINAYE EDGHVVFDIVAYRDNSLYDMFYLKKLDKDFEVNNKLTSIP 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   347 KPLEVFPSMFVTHQLNAFEADDGNFVADMVVYDSHDP----YVKYFYTDFLTKQLYPSTA 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              354 TCKRFVVPLQYDKDAEVGSNLVKLPTSATAVKEKDGSIYCQPEILCEGIELPRVNYDYNG 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44.1 SPPARFERENVITOVVVSEPNKAPFILILDAKTEKELGRATVNVEMHLDLHGMFIFQND 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 FNRNKEEHPEPIKAEVQGQL-----PTWLQGVLL----RNGPGMHTIGDTKYNHWFD 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 FNOTHLGFPEAMDGDKYRELYCPSKNIPKWLDGYFLCQLSASYGNSSAFEGE-KLNHMID 78
                                                                                                                                                                                                                                                                                                                         A;Introns: 51/1, 92/3, 176/3, 235/3, 332/2, 514/1, 543/2, 569/3, 677/1, 732/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.) VDTNGVRRVVGLYDYGVWD---INACGSNDEY---IGDKTLL-PGYIHSITSTENFILLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53 GLALLHSFTFKNGEVYYRSKYLRS-----DTYNCNI------EANRIVVSEFGT
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A;Reference number: 221500
A;Acression: T34293
A;Status: preliminary; translated 1:om GB/EMBL/DDBJ
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[04] VEGALTKHELEBIPLPKTAPPFVQ1 SANFAPVPENPVTQSLT-VTSKLPKOVQGVYVKNGAN 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 ETNETPRIPPQTLETLPRVPYSRYVAVNLATSHPHY---issacintinmatstvipkgrtky 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HHINAY-EELGHVVFDIVAYRDNSLYDMFYLKKLDKDFEVNNKLTSIPTCKRFVVPLQYD-465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3-66 - KIDAEVGSNI VKI,PTSATAVK - - PKIGGSTYGGPF11,GPG1F1 PHVNYDVNGKRYKYVY - - - - 4-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 318 KEVATGOTHTPAPSTLSPVNLHPQSGKVAALFQLLDPHGEFPHVPKDNVGQASKYTYMSG 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 ---ALEVOWSPVPIKIAKLNVOTKEVLH-WGEDHCWPSEPIFVPSPDAKEEDEGVVLLCV 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 VOSGED FUNGSVEL PNSPGMHT FGLERYNHWEICH HSPELHSNIGEVYRSKY FRSDLY 79
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                                                                                                                                                                                                                                  32 ISGNIPEGLPGTLYPNGPAPLERGGMLAGHWFFNNGAILAVNFTDGGVHAFYRYVQTVGY 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39 MHTIGDTKYNHWEDGLALLHSETFKNGEVYYRSKYLRSDTYNCINTEANKIVVSEFGTMAY 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable 9 cis epoxycarotenoid dioxygenase [imported] - potato
C;Species: Solanum Luberosum (potato)
C;Species: Solanum Luberosum (potato)
C;Accession: T51936
R;Burbisge, A., Taylor, I.B., Thompson, A.
Submitted to the EMBL Data Library, March 2000
A,bescription, Potato putalive 9 vis epexycarotenoid dioxygenuse 1 cDNA.
A;Reference number: 225874
A;Reference number: 225874
A;Reference number: 225874
A;Retession: T51936
A;Status; preliminary: translated from GB/FMRL/DDR3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147 -----ALDLQTLETWGEDNLGG--LTNGLTYSAHYKODPOTKETFNFG1SLALNAK
                                                                                                                                                                                                                                                                                                                                                                                           92 QVENTADKFLYGNYG-MTAPGPVWNQWRKPIKNAANTSVLALPDKLLALWEGGRPY
9.4%: Score 264.5; DB 2; Length 472;
12.7%: Fred. No. 4e·11;
Live 72; Mismatches 192; Indels 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.3%; Score 264; DB 2; Length 604; 21.8%; Pred. No. 6.2e-11; tive 94; Mismatches 219; indels if
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A;Cross references: EMBL:AJ276244; FIDN:CAB76920.1
C:Genetics:
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Matches 128; Conservative
                                             Best Local Similarity 12.79
Matches 109; Conservative
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Db 164 -PLPEPTAGPHPPTAGPAWHAVQPKNASASYACPFLETERFVQEKALGPPVF 214		190 DPCKNIEAKAFSYLSHIIPEFIL-NCLINIMPTGDAVYATSETNFIR 145
Qy 99 PDPCKN1FAKA-FSYLSHTIPEFTDN7L1 126	dr.	:
Db 215 PKAIGELHGHSGIAPIMEPYAPGLEGLIDHSROTTGVANAGIVYFNNHIJAMSPIDLEYHV 274	Q7 1	146 FIDEGTERTLEWEYSKYVAVNLAISHPHYD-SAGNILHMGTSIVEKGETKVVLFKIPSS 204
PYYATSETNETEKTEPQTI ETI D		
Dh 275 KVTFTGD	· · · · · · · · · · · · · · · · · · ·	205 VPEREREPSTERRIEVY SEPSEMBERT 1264
ASIPSPELLQPSYYHSPGI1ENY	r QI	385 ISBGERSEDVEIDLIGGERMHIPPALIFINEVI 21
DD 316 YDVIQKPYLKYFRPSKNGEKSNDVEIPVEDPTMMHDFAITEKFV 359	Qy 2	265 RGVNWASCLSFHKEDKTWFHFVDEKTKKEVSTKFY-TDALVLYHHINAYEEDGHVVF 320
NWASCLSFHKEDKTWFHF	Db 4	431 PGGSPVVYDEKKKSPFGILNKNAKDASSIQMIEVPDGFCFHLWNSWEEPETDEVVVI 487
Db 360 IIPDQQVVEKMSEMIPGGSPVVPDKNKVSPPGII,PKYAKDGSDI,KWVEVPDCF 412	Q.Y	321 DIVAYPONSLYDMPYLKKLDKDPEVNNKLTSIPTCKPPVVPLCYDKDAEVGSNLVK1141S +80
OY 305 EXHHINAYEE - DGHVVEDIVAYEDNSLYFMFYLKKLDKLFEVNNKLISIFTCKFFVVP 351	4 da	:::: : :
LWNAWEEPETDEIVVIGSCMTPP		381 ATAVKEKIGSIYGGPFILTF-GIFI PPVNTFVNGKKYRYVATFVQMSPVPTKIAKLNVQ 4.49
OY 362 LQYDKDARVGSNLVKLPTSATAVKEK PASTYPQPELLPEGIELPEGIELPEVNYPYNGKKYKVV 420	, a	VISEQVNI FAGMVNPNILG
RLNLKTGKSTRKAIIENPDEOVNLEAGMVNFNKI	Qy 4	440 TKEVLHWGEDHCWPSEPTFVPSPDAREEDEGVVLTCVVVSEPNKAPFLIIDAKTFKE 497
OY 421 ATEVGWSPVPTKIAKINVQTKEVLHWGEGHGWPSEPIFVF-SFGAPEGFGSVVLTGVV 477	લુ	57]
DD 499 LATAEPWPKVSGFAKVDLFTGEVEKFTYG-DNKYGGEPLFT PFOPNSKEFOWSTIL-AFV 556	Q.Y. 4	448 IGERATVINVEMHLDLHGMFIPQNDIGAE 524
478 VSEPNKAPFILLLDAKTEKELGPATVNVPHH1-1 H5MF1-E-1 NL-L	କ୍ଷଣ	628 EATVILPSEVEYSEHGIFTSETTISE 654
DD 557 HDEKEWISELQIVNAMTLKLEATVKLPSRVPYGFHGTFINANDL 500	RESULT 15	
RESULT 14	JC4324 lignostilbe	ene alphabeta-dioxygenase (EC 1.13.11.43) III isozyme beta chain - Pseudomo
protein F3F9.16 (imported) - Arabidopsis thaltana G.Species: Arabidopsis thaliana (mouse-ear cress)	C,Species: C,Date: 04- C,Accession	Seudomionas paudimobilis -Jan-lyva seeguence_revision v8-Feb-lýva #texi_∽hange 17-Mar-1949 n: JC4324
C:Date: 02-Mar-2001 #sequence_rovision 02 Mar-2001 #texthung- 31-Mar-2001 C:Accession: E96812	F; Fameda, S Biosci, Bio	S : Saburi, Y otechnol Riochem, 59, 1866-1868, 1995
R.Theologis, A., Ecker, J.R., Faim, C.J., Federspiel, N.A., Kaul, S., White, O., Alease, Chin, C.W., Chung, M.K., Cann, L., Conway, A.B., Codway, A.F., Creasy, L.H., Rewar, R., ansen, N.F., Hughes, B., Hülzar, L.	A, Title; A, Pefetene A:Accession	Ayfirle, Cirning of a jignestilbereralla, beta-dioxygenase isotyme jone from Exeudom Ayerterene undan Jedala, Mull Größeri, Pwit 8534977 Asecession: Jedala
	A; Molecule	type: DNA
Aracinota Bander, L. P. Perkins, J., Panas debesed, J., Flod, S., Magkin, E., Kiff, C.A., L. J. H.; I.I. Y. Lin, X.; Liu, X.; Liu, Z.A., Lures, T.S., Maiti, P., Marviali, Rizzo, M., Romeey, T., Rowley, D., Sakano, H.	A, Resilles. A, Experimen A, Note: the	. 1 487 EAM> - Intalsource TMYTO09 e translation initiation codon AIG is not given in this paper
A/Authors: Saltberg, S.L., Schwartz, T.F., Shinn, P., Scothwick, A.M., Sun, H., Tallon, Ker, M., Wu, D.; Yu, G., Fraser, C.M., Venter, J.C.; Davis, F.M. A. Title Common and A. Davis, C. M. Marillo Common and A. Title C. Title Common and A. Title Common and A. Title Common and A. Title Common and A. Title C. Title C. Title Common and A. Title C. Title	C.Comment C.Genetics:	This energies is significant in the metabolism of dimeric lightin compounds.
Attoric Segarate and analysis of enfonceour 1 of the plant Arabidopsis. Africance sumbor: A8f141; MUTD:21016719; PMID:11130712 A:Accession: E96812	A;sene: isc C;Keywords.	nb . oxidoreductase
A:Status: preliminary A:Status: preliminary A:Status: preliminary A:Status: preliminary	Query Match Best Local a	8 7%; Scott 245.5; PR 2; Longth 480; Stmilarity 22.4%; Pred. No. 9.46-10;
A. residues. 1.16.7 (1.5.1). A.Cross references: GB: AE(ii)5173; NID: g80,52543; PII:N·AAF71797.1; GSPUB.:GN00141	Matches	iil, Conservative 75, Mismatches 211, indels 141: Japs 22:
C,Genetics. A,Gene: F3F9.10	22	19 EVGEGETPIMEGEVELPNEIGEMITGEFRYNBWEIGEALALTHEFTFRYGFYYFSKYLKSDT 78
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Cuery Match Cuery Match Best Local Similarity 22.9%; Pred No. 1.1e-10; Matches 130: Conservative 87: Mismatches 220; rado's 121: Cans 26:	5 6	79 YNCNIEANRIVVSEFGIMAYFEFGENERARFSYLSHTHENTISHIH HE 128 BE GYVERARAN - STIFE - AVENIE
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Qy 41 TIGDTKYNHWFDGIALLHSFTFKNGFVYPSKYIRSDTYNGNIEANPIVVS-EBGTMAVP 99	27	PSSVPEKEKKKSCFKHLEVVCSI
SCMVHAVEFT	45	133 ALCELLIDOSYFELD PADALLELIH QVEVYOMMENY 20

VWAS	221 LTEHYAIPHIVPGSPNWPBLKAGLPHPGFDTTLPVWLGVVPRGPGVTNKDVRW 273	297 KFYIDALVLYHHINAYEEDGHVVFDIVAYEDNSLYDMFYLKKLDKDFEVNNKLTSIPTCK 356	274 FKAPKTIFASHVMNAFEEGSKIHFUTPQAENNAFPFFPDIHGAPFDPVAA 323	VKLPTSATAVKEKIMS	324 RPYLHRWIYOLGSNSEDFAEVKQLTSWIDEFPRVDARYVGQP 365	416 YKYVYACWPSEP 456	16 YRHGWGLVMDPEMEMEFARGRASGFKMNRIGHWDHATGKEDSWWCGPQSILQEP 419	457 IFVPSPDAREEDEGVVLTCVVVSEPNKAPFILLIDAKTFKELGRATVNVEMHLDLHG 513	420 CFVPRMADSAPCINTYTIALVDNITTNYSD-IVVLDALNLKDGPIGPAKLDIRLKSGLHG 477
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GenCore version 5/1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

July 15, 2003, 09:05:54; Search time 24 Seconds (without alignments) 909.023 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-10-053-192-1 2825 1 METIFNRNKBEHPEPIKAEV...... MHLDLHGMFIPQNDIGAETE 526

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 scqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result		Query		6		
. O	score	Match	Length	DB :	ID	Description
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17	103	3.6	804	7	SCY1_YEAST	
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C1	101.5	33	1447	_	BUD4_YEAST	P47136 Saccharomyc
53	101.5	ۍ ص.	3712	-		Q60174 drusuphila
C4	101	3.6	297	_	T257_ECOLI	
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GYPR_MYCGE	XPKA_LACPE	SYL1_SULSO	2208_HUMAN	MY HA_RAT	RPNS_SCHPO	YB79_YEAST	SERA_PLAFG	MSN5_YEAST	YK28_BORBU	AKT3_RAT	SLM9_SQHPO
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ALIGNMENTS

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1034 HIIGVDKPTEDIYAEVWADGLTNSTGOGPNMIAQLGY-KYVSGTV-----YDSVYGSVY 1086
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Multifunctional enzyme; Glycoprotein.
SIGNAL 1 35
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FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
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                                 PF02806; alpha-amylase_C; 1.
FF02903; alpha amylase_N; 1.
PF02922; isoamylase_N; 1.
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PF00128; alpha amylase; 1. PF00395; SLH; 3.
                                                                                  SMART; SM00060; FN3; 1. PPOSITE; PS01072; SLH_DOMAIN; 3.
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Phosphate regulating neutral endopeptidase (EC 3.4.24..)
(Metalloendopeptidase homolov FEX) (X-linked hypophosphatemia protein)
(HYP) (Vitamin D-resistant hypophosphatemic lickets protein).
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MEDLINE.9024647, PubMed=7550399,
MEDLINE.902024647, PubMed=7550399,
Lehrach H. Rowe P.S. Korn B. Renhardt R., de Jong P., Poustka A.,
Lehrach H. Rowe P.S. N. Goulding T. N. Summerfield T. Monutford P.,
Read A.P., Popowska E., Pronicka E., Davies K.E., Oriordan J.L.H.,
Read A.P., Popowska E., Pronicka E., Davies K.E., Oriordan J.L.H.,
Hanauer A., Strom T.M., Meindl A., Lorenz B., Caqnoli M.,
Mohnhike K.L., Murken J., Meindl A., Lorenz B., Caqnoli M.,
M. Agene (PEX) with homologies to endopeptidases is mutated in
Patients with X-linked hypophosphatemic rickets. The HYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Expression and cloning of the human X linked hypophosphatemia gene
                                                                                                                                                                                                                                                           Francis F., Strom T.M., Hennig S., Boeddrich A., Lorenz H., Brandau O., Mohnike K.L., Cagnoli M., Steifens C., Klages S., Bozzym K., Pohl T., Oudet C.L., Econs M.T., Powe P. S. N., Peinhardt Mettinger T., Lehrach H.; "Genomic organization of the human PEX gene mutated in X-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beck L., Soumounou Y., Martel J., Krishnamurthy G., Gauthier C., Goodyer C.G., Tenenhouse H.S.; Goodyer C.G., Tenenhouse H.S.; Terex/PEX tissue distribution and evidence for a deletion in the 3' region of the Pex gene in X-linked hypophosphatemic mice."; J. Clin. Invest. 99:1200-1209(1997).
                                                                                                                   Edkaryola, Metazoa, Chordata: Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                      SEQUENCE FROM N.A., AND VARIANTS HYP ARG-85; LEU-544; ARG-579 AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lipman M.L., Panda D., Henderson J.E., Shen Y., Goltzman D.,
Karaplis A.C.;
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Thakker R.V., Schlessinger D.;
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15-JUN-2002 (Kel. 41, Last annotation update)
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Genome Res. 7:573-585(1997).
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MEDLINE-97343325; PubMed-9199930;
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MEDI.INE-9723252; PubMed-9077527;
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MEDLINE=97343443; PubMed=9199999;
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DEFORMITIES, GROWTH PAILURE, CPANIOSYNOSTOSIS, PARAVERTERAL.
ACALCIRICATIONS, PARUDOFRACIOURES IN LOWER EXTREMITIES, AND MUSCULAR
HYDOTONIA WITH ONSET IN EAKLY CHILDHOOD, X-LINKED HYPOPHOSPHATEMIC
RICKETS IS THE MOST COMMON FORM OF HYPOPHOSPHATEMIA WITH AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FETAL HERRY, LUNG, LIVER, AND KIDNEY.
DISEASE: DEFECTS IN PHEX ARE A CAUSE OF X-LINKED HYPOPHOSPHATEMIC PICKETS (HYP), A DOMINANT DISORDER CHARACTERIZED HY IMPAIRED
                                                                             WARIANTS HYP SER-77; PRO-138; LEU-534 AND ARG-579.
MEDLINE=9752387, PubMed-9297956;
PROWE P.S.N., Oudet C.L., Princis F., Sinding C., Fannetier S.,
ECONS M.J., Strom T.M., Meitinger T., Garabedian M., David A.,
Macher M.-A., Questiaux E., Popowska E., Frontcka E., Read A.P.,
Mokrycki A., Glorieux F., Popowska E., Frontcka E., Read A.P.,
Goulding J.N., O'Riordan J.L.H.;
Pisstributhon of mutations in the PEX gene in families with X-linked
Hum. Mol. Genet. 6:559-549(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Directstant hypophosphatomic estromalacia, evidence that the discrebed is not a distinct entity from X-linked hypophosphatomic rickers ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dixon P.H., Christie P.T., Wooding C., Trump D., Grieff M., Holm L.A. Gertner T.M., Schmidtke T., Shaw N., Smith C., 199 C., Schlessinger D., Whyte M.P., Thakker R.V., "Matchising analysis of PHEX gene in X linked hypophosphatemia."; J. Clin Endocrinci Metab. 83:3615-3623(1998)
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TISSUE SPECIFICITY: LYMPHOCYTE AND FETAL BRAIN; NOT IN ADULT
BRAIN, PLACENTA, SKELETAL MUSCLE, AND PANCPEAS; NOT IN ADULT AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANIS HVP P-317; 1-534; P-579; R-521; N-580 DFT, T-720; Y-731 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHATE UPTAKE IN THE KIDNEY, WHICH IS LIKELY TO BE CAUSED BY ABNORMAL REGULATION OF SCOTOM PHOSPHATE CUTRANSPORT IN THE PROXIMAL TUBULES CLINICAL MANIFESTATIONS INCLUDE SKRUETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-20451419; PubMed-11004247; M. Asikuru Y., Firbibana P., Sabte F., Tajima T. Nakae T., Adaddim M., Asikuru Y., Firbibana P., Suwa S., Katsumata N., Tanaka T., Hiyashi Y., Abe S., Murashita M., Okuhara K., Shinohara N., Fujieda K.; Three novel PHEX gene mutations in Japanese patients with X-linked hypophosphatemic rickets."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: PPORARIY INVOLVED IN RONE AND DENTIN MINERALIZATION AND RENAL PHOSPHATE REABSORPTION.
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"Non-random distribution of mutations in the PHEX gene, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-984305R2; Pubmed-9768645;
Econs M.J. Friedman N.E., Rowe P.S.N., Spear M.C., Francis P.,
Strom T.M., Oudet C.L., Smith T.A., Ninomiya I.T., Loc B.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Identification of fifteen novel PHEX gene mutations in Finnish patients with hypophosphatemic rickets "; Hum. Mutat. 15:383-384(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARTANTS HYP S-80; F-142; G-237; G-530; F-573; S-733 AND W-745; MEDLINE=99368844; PubMed=10439971;
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Eur. J. Hum Genet 7:615-619(1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "A PHEX gene mutation is responsible for adult-onset vitamin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARTANTS HYP F-85; P-141; V 341 DEL, P 567; K-680 AND Y-693.
MEDLINE=20202840; Pubmod-10737991.
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J. Hum. Genet. 60:790-797(1997)
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    SIMILARITY: PELGNGS TO PEPTIDASE FAMILY M13.
    FATABRASE, MAME THEATH, WWW "Entp.//doi.org/mod/finespill.com/phosoily.".

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EMBL; U75645; AAB47749.1; -.
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Y08117;
Y08118;
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YOB127;
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Y08129;
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4.34 MMEELVEGVRWAFIDMLEKENE----WMDAGTKRKAKEKARAVLAKVGYPEFIMNDTHVN 4.89
                                     411 AYEEDGHVVFDIVAYRDNSLY-----DMFYLKKLDKDFEVNNKLTSIPTCKRFVVPL 362
                                                                              490 -- EDLKAIKFSEADYFGNVI,QTRKYLAQSDFFWLRK------AVPKTEWFTNPT 535
                                                                                                                                                             346 TVNAFYSASTNQIRFPAG-----ELQKPFFW-----GTEYPRSLSYGAIGVIVGHEFT 583
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                                                                                                                        46.3 OYDKDARVGSNLVKLPTSATAVKEKDGS1YQQPE11.CEG1ELPRV--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete nucleotide sequence of Sancharamyoes serevisiae chromosome
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01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1998 (Rel. 36, Last almulation update)
Hypothetical 143.6 kDa protein in SPOI6-FEC104 intergenic region.
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Saccharomycetales, Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
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PROSITE; PS50003; PH_DOMAIN; 1.
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InterPro; IPR001849; PH.
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STPAIN S2880 / AB972;
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58 HSFTFKNGEVYYKSKYLKSDLYNGNIEANKLVVSEFGIMAYFDFCKNIFAKAFSYLSHTI 117

150; Indeis 151; Gaps

Pred No 4 3; Mismatches

18 8%:

Best Lucal Similarity 18 8 Matches 88; Conservative

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78:

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571. YPYSLKVIPPIQERSIPF-SVNHPFLQVPKFLVLLPYSSVWPPNNKGKFASMAFVTI NHTV-629
                                                                  118 PEFTDNCLINIMKTGDDYYATSETNFIRKIDPQTLETLDKVDYSKYVAVNIATSHPHYLS 177
                                                                                                                SPIKHVSS 562
                                                                                                                                                                                                         663. RMLHMQRGIGLEFNMSVFFIDREAVASKLQFEIENKAMHIPRGERFVLFIFQELDFFIFN 722
                                                                                                                                                                                                                                                        ** KEDIVKEATA 262
                                                                                                                                                                                                                                                                                                    723 EKKLIKDNLSESEHYSKDYDYLLKSTYDHHFENTN-----FTPMFLMSKKLRLRERFAMC 776
                                                                                                                                                                                                                                                                                                                                                  263 YIPGVNWASCLSFHKEDKTWFH--FVDPKTKKEVSTKFYTDALVL------ YHH 408
                                                                                                                                                                                                                                                                                                                                                                                               777 YFQD-----NFKVGSKTLFHVLFGDK-----SQVFPSSLFLCKKGSNLNNNSYWER 822
                                                                                                                                                                                                                                                                                                                                                                                                                                           309 INAYEEDGHVVFDI-----VAYRDNSLYDMFYLKKLDKDFE--VNNKLTSIPTCKKFV 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360 VPLQYDKDAEVGSNLVKLPTSATAVKEKDGS1YCQPE1L,------CEG1ELPR -- 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Engert J.C., Berube P., Mercier J., Dore C., Lepaue P., Ge B., Merdard J.-P., Mathieu I., Melanen S.R., Schalling M., Lander E.S., Morgan R., Hudson T.J., Richter A.; "AfSACS, a speakler ataxia common in neatherstern Quebec, is caused by mutations in a new gene encoding an 11 5-86 ORF.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPANIE ATAXIA OF CHARLEVOIX-SAGRENAY (AFSA'S OF SA'S), AKSACS IS
AN EARLY ONSET NERPODEZENERATIVE DISPASE WITH HIGH PREVALENCE IN
THE CHARLEVOIX-SAGRENAY-LAC, SAINT-JEAN REGION OF ORDHREC, IL IS
CHARACTERIZED BY ABSENI SENSORY-NERVE CONDUCTION, REDUCED MOTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       823 IRRAKEDASCOFELCRKLOFOLNRTSNFIKDLLWLKDDNDNFKLVLOPPVTKIKU----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XI. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
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                                                                                                                                                             178 A-----GNILNMGISIVDK----GRIKYVLHKIDSSVPEREKK-KSCHRHER-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Verfebrata, Eufeleustomi;
Mammalia, Futberia, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISEASE: DEFECTS IN SAME AND THE CALLS OF ANYONE DEFENSIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: MAY FUNCTION IN CHAPERONE-MEDIATED PROTEIN FOLDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          !- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE CENTRAL NERVOUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nagase T., Ishikawa K. I., Suyama M., Kikuno R., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              407 -- VNYDYNGKKYKYVYATEVQWSPVPTKIAKLNVQTKEVLHWGEDHC 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KINTEVERIMI, FERTHINMALLY 959
                                                                                                                                                                                                                                                        220 ---VVCSIPSRS------LLQPSYYHSF0IIENYIVFIEQPF--
                                                                                                            ----YUNISGESYLRKID---LIDIDSLEYDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lh-(MCF-2001 (Rel 40, fast sequence update)
16-0CI-2001 (Rel 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FPOM N A , AND VARIANT ALA-2619.
MEDLINE-20120709; Pubmed-10655055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPT:
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MEDLINE-99087487; PubMcd-9872452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 2826-3829 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SACS_BUMAN STANDARD; F
Q-9NZJ4, 094835;
U-9CM-2401 (Red 40, Created)
In-0CM-2401 (Red 40, Inst Sequ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .606 SEKVSFHL------NFEAAPYLYQLPNKYKNNFRELFETVGVKQSCTVEDFALV 1653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .654 LESIDQERGTKOTTERNFOLCPRISEGIWSLIREKKOEFCEKNYGKILLPDINLMLLPA 1713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1769 GTEFGOKEKLISRIKSIL----NAYPSEKEMLKELLONADDAKATEICFVFDPROHPVD 1823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1523 SVSLAVKEFLGLLKKPTVDLVINQLKEVAKSVDDGITLY------QENITNACYKY 1572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1573 LH------EALMONE-----ITKMSIIDKLKPFSFILVE--NAYV------D 1605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1824 RIFDDKWAPLOGPALCVYNNOPFTEDDVRGIQNLGKGTKEGNPYKTGQYGIGFNSVYHIT 1883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 AVNLATSH-----PHYDSAGNILNMGTSIVDKGRTKYVLFKIPSSVPEKEKKKSCFKH 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218 LEVVCSIPSRSLLQPSYYHSFGITENYIVFIEQPFKLDIVKLATAYIRGVNWASCLSFHK 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        278 EDKTWFHFVDRKTKKEVSTKFYTDALVLYHHINAYEEDGHVVFDIVAYRDNSLYDMF--Y 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----FEVNNKLTS-----IPTCKRFVVPLQYDKDAEVGSNLVKLPT 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     480 -----EDNKAPFLLIIDAKTFKE------LGRAT------VNVEMHLD 510
                                                                                                                                                                                                                                                                                                                                                                                 430 PTKIA----KLNVQTKEVLHWGEDHCWPSEP1FVPSPDAREEDEGVVLTCVVVS-----
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NEPVE VELOCITY AND HYPEPMYELINATION OF RETINAL-NERVE FIBERS. SIMILARITY: CONTAINS 1 J DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.9%: Score 110 5; PR 1, Length 3829;
20.4%: Fred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3829 AA; 436972 MW; 7AE990311E1E3E91 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 20.4%: Fred. No. 20;
Matches RR, Conservative 62; Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-1989 (Rel 10, Last sequence update)
16-m<sup>ort</sup>-2001 (Rel 40 (ast anaptation update)
Hypothelical 259 kTo proteis yof2 (OPP 2136)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V -> A.
/FTId=VAR 010296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ThierPro; [PPGG1623: ShallN
PROSITE: PSG0636: DNALL: FALSE_NEG.
PPOSITE: PSSG076; DNALL2: 1.
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DOMAIN 3556 3643
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P09975;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 NGEVYPSKYLPSDTYNCNIEANPIVV-----SFFGTMAYPDPCKNIFAKAFS 111
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Eukarycta; Viridiplantae; Streptophyta; Embryophyta; Marchantiophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78; Mismatches 143; Indels 127; Gaps
                                                                                                                                                                                                                  Ohyama K., Fukuzawa H., Kohchi T., Shirai H., Sano T., Sano S.,
Umesono K., Shiki Y., Takeuchi M., Chang Z., Aota S., Inokuchi H.,
                                                                                                                                                                                                                                                                                                                       "Chloroplast gene organization deduced from complete sequence of
                   Marchantiopsida, Marchantiidae; Marchantiaies; Marchantiineae;
Marchantiaceae; Marchantia.
NCBL_TaxID=3197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.8%, Secretion 5, DR 1, Length 2136; 19.1%; Pred. No. 13;
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SEQUENCE 2135 AA; 259911 MM; 5BD1700900761197 CR064;
                                                                                                                                                                                                                                                                                                                                                              liverwoit Marchantia polymorpha chloroplast DNA.";
Nature 322.572-574(1986).
-!- SIMILARITY: BELONGS TO THE YCF2 FAMILY.
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PIR, S01591; S01591.
InterPro, IPR0030909, AAA_ATBase_centr.
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nes 82; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.96 ANUSIRUMS) OF 1171-1304
MEDLINE-99170415; PubMed-10078829;
Vetter I.R., Nowak C., Nishimeto J., Willinghofer A.;
"Structure of a Ran-binding domain complexed with Ran bound to a GTP
                                                                                                                                                                                NEULINE=95294031; PubMed=7775481; MEDLINE=95294031; PubMed=7775481; Mu J., Matunis M.J., Kraemer D., Rlobel G., Coutavas E.; Nu J.S., Matunis M.J., Kraemer D., Rlobel G., Coutavas E.; Nu J.S., a cytoplasmically exposed nucleopoin with peptide repeats, Ran-GTP binding sites, zinc fingers, a cyclophilin A homologous domain, and a leucine-rich region.":
J. Biol. Chem. 270:14209-14213(1995).
             Ran-binding protein 2 (Ransh2) (Naclear pare complex protein Nupaca)
(Nucleoporin Nupasa) (358 kDa nucleoparin) (F276).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 398:39-46(1999).
                                                                                                   Eukaryota, Metazoa, Chordata, Graniata, Vertebrata, Esteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                              MEDITNF-96-327194; PubMed-7603-52;
Yokoyama N., Hayashi N., Seki T.,
Kuma K.I., Miyata T. Fukui M., Nishimoto T., Pante N., Aebi H.;
"A qiani mucleopore protein that binds Han/Tr?4";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - DOMAIN: CONTAINS F-X-F-G REPEATS.
- SIMILARITY: CONTAINS 4 RANBOL DOMAINS.
- SIMILARITY: CONTAINS 8 RANBOL-TYPE ZINC FINGERS.
- SIMILARITY: CONTAINS 8 RANBOL-TYPE ZINC FINGERS.
- SIMILARITY: CONTAINS 1 CYCLOPHILIN-FIRE PPIASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           implications for nuclear transport.";
(2002 (Re) 41. Last amsoration update)
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SMART, SMOR47, 7DE_RR2, 8
PROSITE; PS00170; CSA_PPIASE_1; 1
PROSITE; PS50072; CSA_PPIASE_2; 1.
PROSITE; PS50196; RANBD1; 4.
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InterPro: IPR00069; RanHPl_WASP.
InterPro: IPR000156; Ran_HPl
InterPro: IPR001440; TPP
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                                                                                   Homo sapiens (Human).
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                                                           KANBP2 OR NUP358.
                                                                                                                                               N'BI_TaxID=9606;
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267 VNWASCL-----SFHKEDKTWFHFVDPKT--------KKEVSTRFYTDALVL 305
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FROSITE, PSG1379, ZF_MANNP2_1; 8.
PROSITE, PSG3199, ZF_MANNP2_2; 8.
Nuclear protein, Transport, Repost, Zinc finger, Isomerase: Rotamase:
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Zhao S. Mitchell S F. Meng J., Doyle M P., Kresuvich S.;
"Cloning and sequencing a gene associated with an outer membrane
protein of Escherichia coli 0157:H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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MPDLINE=21074034; PubMed-11206551;
Perna N T , Plunkett G III, Puthland V , Mau B , Glasner J.D.,
Posta D J., Maybew G F , Evans P S , Gregor I , Rickpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
                                                                                                                                                                                                                                                                                                                                                                                                                      3.8%; Score 108.5; PB 1; Length 4224;
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7 R -> H (IN REF. 2).

14 R -> K (IN REF. 2).

359214 MW. 54E78412C36A3C3 CEC64;
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(Rel. 41, Last annotation update)
                                                                                                 KANBP2 - TYPE 1.
RANBP2 - TYPE 2.
RANBP2 - TYPE 4.
RANBP2 - TYPE 4.
RANBP2 - TYPE 5.
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RANBP2-TYPE 7.
RANBP2-TYPE 8.
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YHBX OR 24535 OR ECS4053.
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16-OCT-2001 (Rel. 40, Last sequ
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3067 322
777 77
784 78
3224 AA,
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P58216;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 NGEVYYRSKYLRSDTYNCNIEANRIVVSEFGTMAYPDPCKNIFAKA-----FSYLSHTI 117
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                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Appdaca J. Anantharaman T.S., Lin T., Pen G., Schwartz D.C., Welch R.A., Blattner F.R., "Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
                                                                                                                                                                                                                                                                          :H7 and genomic comparison with a laboratory strain K-12
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60639 MW; B9C140B660FA0ER9 CPC64;
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EMBL; AP002564; BAB37476.1; ALT_INIT.
Interpro; IPR003371; DUF146.
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                                                                                                                                      STRAIN=0157:H7 / RIMD 0509952;
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between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                       16-0CI-2001 (hel. 40, Last sequence update)
16-0CI-2001 (hel. 40, Last annotation update)
RNA-polymerase-associated transcription specificity factor (PAP94)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20193820, FubMed-18729156,
Afonso C.L., Talman E.R., In 7., Esak L., Kutish G.F., Rock D.L.,
"The genome of fowlpox virus.";
J. Virol. 74:3815-3831(2000)
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InterFig., IPRG04974, Pox_Rap94.
Pfam. PFN7294, Pox_Rap94, 1
Transcription; Late protein.
SEQUENTE 794 AA; 95120 WW; DAYED21453537BD3 CRC64;
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21 8%; Prod No 4
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Andiname ALO., Celniker S.E., Holt R. A., Sahayara A., Chen L.X.,
A. Sutton G.G., Worthan J. F., Vandell M. D., Zhang Q., Chen L.X.,
A. Brandon K. C., Baxter E.G., Helt G., Nalson C. R., Mikhos G.L.G.
A. Abril J.F., Aqbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
Besson K.Y., Benge B. V. Farman B.P., Rhandari D., Bratter P. M.
Besson K., Doup L.E., Downes M., Davenport I. R., Distakov S.,
A. Cherry J. M., Cawley S., Dahlke C., Davoport I. R., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dadan-Rocha S., Dunkov B.C., Dunn P.,
A. Dodson K., Doup L.E., Downes M., Dadan-Rocha S., Dunkov B.C., Dunn P.,
A. Dodson K., Doup L.E., Downes M., Dadan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dadan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dadan-Rocha S., Dunkov B.C., Dunn P.,
RA Brin D., Houston K.A., Hermand S.J., Harris M.,
A. Harrye N. L., Harryey D., Helman T.J., Harrandoc J.R., Hackin M., Cabilelian A. C., Ferrar C., Perriard S., Panaris M.,
A. Harryey M., Marlosh F., Rarpen G. H., Kraft C., Merjan P., Harris M.,
A. Lasko P., Lei Y., Levitsky A. A., Li J., Li Z., Liang Y., Lin X.,
A. Lasko P., Lei Y., Levitsky A. A., Li J., Li Z., Liang Y., Lin X.,
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A. Murkulov G., Milshina N.V., Mobarry C., Morbor S., Morber S., Shen H.,
A. Spier E., Spradling A.C., Stapleton M., Strong R., Sun R.,
A. Spier E., Spradling A.C., Stapleton M., Strong R., Sun R.,
A. Wang B.C., Sidon-Kiamos I., Singsul M., Shug S., Ran Y., Walssenbach J.,
A. Wallshe R.C., Sidon-Kiamos I., Singsul M., Shug S., Ran Y., Walssenbach J.,
A. Walliams S.M., Wooday F. W., Weilsenbach F., Sidon V., Walsker M., Wooday E., Walssanman D.A., Weilsenbach S., Sidon-Kamanos J., Shug S., Shu Drosophila melanogaster (Fruit, fly).
Rusuryota Metazou, Arthiopoda, Mandibalata, Fanciustacea, Hexapoda, Inserta, Pteryyota Newptera: Foloppertyyeta: Diptera; Brachycera; Muscomorpha, Ephydroidea; Brosophilidae; Drosophila. Champe M., Chavez C., Dorsett V., Drosnok D., Furfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller R., Li P.W., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Herold A., Klymenko T., Izaurralde E., "NXF1/pl5 heterodimers are essential for mkNA nuclear export in , Brokstein P , Hong [. Agbayani A., Parlson J [5-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Pr.! 41, Last Sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) MEDLINE=21638995; PhbMed-11780633; MEDI.INE=20196006; PubMed=10731132; Nuclear RNA export factor 2. 389 YNKSIFMSEPY 399 STANDARD: RNA 7-1768-1780(2001) SEQUENCE FROM N.A. SEQUENCE FROM N.A. SECUENCE FROM N.A. STRAIN-Borkeloy; NCB1_TaxID=7227; NXF2 OR CG4118 Stapleton M. 15-JUN-2002 15-JUN-2002 NXF2_DROME Q9VV7 3; Drosophila. NXF2_DROME RESULT 9

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              417 DPE--ECLUKAVSQCYVAQNKMENLEKPHSKEGEKIDVMVSL,SSPKTL,FYVL,----SVAS 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OFF LIPSPARIS :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  564 LOTINPGOSLOKNFLCDT-----GAYELVG-----AFLEN----- YLREFENDEFR 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 -----KNIF--AKAPSYLSHTIPEFIDNCLINI-MKIGD---DYATSFTNFIRK--1-147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148 DECILEMENTAVOYSKYVAVNIALSPPHYDSAGNII NMOLSIVOKORIKYVERIPSSVPE 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            470 RKEMTTCSFTRICHRKVINIAGAHVIJGMMSCLEAVFLSHNWVQDLSSTHSLANLIKSLV 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231 QPSYYHSPGITENYIVFIEQPFELDIVKLATAYIRGVNWASCLSFHKE---DKTWPHFVD 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    530 ----LHGNKLCRNY-------PILPSFYVBAV------KEVFPQLITTLIGVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                324 HW-----HAFMIPDPSHEFNGEVFFPFFFFFFLDP----------TLSNFYPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               288 PKTK - KEVSTKEYTOALVLYHHINAYEED 3HVVED IVAYEDNSLYIMEYEKKLDKD 👵

    FEVELOPMENTAL STACE: Expressed throughout embryceic fevelopment.
    MISCELLANDOGS, THE ENA-Einding demain is a mon canceleal PMP type

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Patel S , Phouanenavong S , Wan K H , Yu C , Lowis S F , Pubin G.M., Celniker S.,
                                                                                                    -!- FUNCTION: May be involved in the export of mRNA from the nucleus to the cytoplasm.
                                                                                                                                                                                            -1- SUBCELLULAR LOCATION: Localized in both the nucleoplasm and the cytoplasm. Not detected at the nuclear rim.
-1- TISSUB SPECIFICITY: Expressed ubiquitously.
-1- IEVERGHERINAL STARE: Expressed throughout embryceic levelopment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam, PF00550; LRR; 1.
PROSITE; PS50177; NTF2_DOMAIN; 1.
Transport; mRNA transport; Nuclear protein, RNA binding, Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PNA-RINDING (PPM) (RV SIMILADITY).
LPR 1.
LPP 2.
LPP 3.
LPP 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 107; DB 1; Length 841;
                                                                           Submitted (JAN-2002) to the FMHL/GenHark/HURL databases.
                                                                                                                                                                                                                                                                                                                                                                                                     SIMITARITY: CONTAINS 4 LEUCINE-RICH REPEATS (LRR). SIMILARLIY: COMIAINS 1 NIEZ DOMAIN. SIMILARITY: CONTAINS 1 PNA RECOGNITION MOTIF (PPM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UBA-LIKE (BY SIMILARITY).
581CE5BUC57FFU98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZÜR KEKKKSCPK----HIRVV------
                                                                                                                                                                                                                                                                                                                                                                               -! - SIMILARITY: BELONGS TO THE NXF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leucine-rich repeat; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY CONTAINS 1 URA DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NTF2.
                                                                                                                                                                Interacts with NXT1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AJ312282; CAC41644.1; -: EMBL, ARG035227; AAR447.1; -: EMBL, AY0705582; AAL68387.1; -: FlyBase; FBqn0036640; CG4118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95634 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterProj IPPGG1611; LRP.
InterProj IPPGG18603; LRPCap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93; Conservative
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548
579
758
831
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524
554
585
788
841 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                           - !- SIMILAPITY:
                                                                                                                                                                   SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                      domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
SEQUENCE
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.ish-sib.ch/announce/
or send an email to license@ish-sib.ch)
----FEVNNKLTSIPTCKRFVVPLQYUKDAEVGSNLVKLFISATAVKEKD----- 388
                                         -i- FUNCTION: DNA POLYMÉRASE III IS A COMPLEX, MULTICHAIN ENZYME RESPONSITE FOR MOST OF THE REPLICATIVE SYNTHESIS IN BACTERIA.

THIS DNA POLYMERASE ALSO FYHIRITS 3 TO 5' EXONGLEASE ACTIVITY.

THE ALPHA CHAIN IS THE DNA POLYMERASE (BY SIMILARITY).

-i- GATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAINS) THAT ASSOCIATES WITH A TAU SUBUNIT WHICH ALLOW THE CORE DIMERIZATION TO FORM THE POLITY COMPLEX POLITY ASSOCIATES WITH THE GAMMA COMPLEX, COMPOSED OF CHAINS GAMMA, DELTA, DELTA', FSI, AND CHI) AND WITH THE BELL OF CHAIN SHILLARITY.

SUBCELLULAR LOCATION. CYLY LASHIC (BY SIMILARITY).

SIMILARITY. BELONGS TO THE DNA POLYMERASE IYPE-C FAMILY. DNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Fleischmann P.D., Ketchum K.A., Klenk H.-P., Gill S., Deugherty B.A., Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S., Loftus B., Richardson D., Dedson P., Khalak H.G., Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson D., Kenley J.M., Cotton M.D., Weldman J.M., Fujil C., Bowman C., Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONTAINS A CORF (COMPOSED OF ALPHA, PPSILON, AND THEIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helirobacter pylori (Campylobacter pylori).
Bacteria; Froteobacteria; epsilon subdivision, Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transferase, DNA-directed DNA polymerase; DNA replication, Complete proteome.
SEQUENCE 1211 AA: 138052 MW: FR2480DA7F4FRROF TREE4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1211 AA; 138052 MW; FR248DE47E4CEBOr CRC64,
                                                                                                                                           389 -GSIYCQPEILCEGIELPRVNYD------YNGK 414
                                                                                                                                                                                                       661 FGCTYI-VEIL---LQLPRVTHDFHSLQTDVMHYNGK 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DNA polymerase III alpha subunit (EC 2.7.7.7)
                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1211 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-97394467; Pubmcd=9252185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003141; PHP_N.
InterPro; IPR004805; PolC_alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1947 (Pel 45, Created)
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TIGRFAMS; TIGR00594; polc; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE000646: AAD08502.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / ATCC 700392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro, IPR004013, PHP_C.
                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pylori.";
Nature 388:539-547(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Piam; PF02231; FHF_N; 1.
Piam; PF02811; PHP_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - (DNA)(N)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNAE OR HP1460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                        DP3A_HELPY
P56157;
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                                                                                                                                                                                                                                                                                                                        RESULT 10
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                                                               21;
                                                                                                                                                                                                                       155 NP----KYGAKGY-DEAKKI---ACEYOF----1FEDDFYLEIMRHG-----ILDQPFID 197
                                                                                                                                                                                                                                                                145 PKIDPQTLETLDKVDYSKYVAVNLATSHPHY-----DSAGNIIMMGTSIVDKGPTKY 196
                                                                                                                                                                                                                                                                                                        198 EQVIKMSLETGLKI------IAŦNDTHYTMPNDAKAĢEVAMCVAMGKTLNDKGKLKH 248
                                                                                                                                                                                                                                                                                                                                              197 VLFKIFSSVPEKEKK--KSCFKHLEVVCSIFSRSLLQ------FSYYHSFGITENYI 245
                                                                                                                                                                                                                                                                                                                                                                                    249 SVHEFYIKSPEEMAKLFADIPEALENTGEIADKCVLEIDLKDDKKNPPTPPSFKFTKAY- 307
                                                                                                                                                                                                                                                                                                                                                                                                                            246 VETEQPFKLDIVKLATAYIRGVNWASGLSFHKEDKTWFHFVGHETKKEVSTKFY1DALVL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----AQNECLNF-----EDDASYFAYKARESLKE------RLVL 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         306 YHHINAYEEIBAHVVPDIVAYEDBASIXIMFYLKKIJIK DFEV INNKLIS-----IPTC 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               337 V---------KERHDQ-YKERLEKFIEVITNMKFD3YMLIVWDFIPYA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         356 KPFVVPLOYDKDAEVGSNLVKLPTSATAVKEKLGSIYCQPEILCEGIFLPPVNYDYNGKK 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              376 KEMGIPVGPGRGSAAGS-LVAFALKITDIDPLKYDLLFERFLNPERISMPDIDTDFCQRR 434
                                                                                                                                           95 KNOEGYENLMELSSMAYLEGFYYFPPINKKLLKEHSKGIIASSAGIOGEVNYHLNTNNER 154
                                                                                                                                                                                   86 NRIVVSEFGIMAYPDPCKNIFAKAFSYLSHIIPEFTDNCLINIMKTGDDYYAISETNFI- 144
                                                                                                       ---YNCNIEA 85
                                                               60; Mismatches 157; Indels 136; Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Through Section 115.441-1004(2002).
-i- FUNCTION: May be involved in transferrin trafficking likely to
power actio-based membrane trafficking in many physiologically
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Worliguez O.C., Cheney R.E.;
"Human myosin-Vc is a novel class V myosin expressed in epithelial
cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutiaria, iramates, Catarrhini, Hominidae, Homo.
                     Sease 197, DB 1, Length 1211;
Pred No. 7,5:
                                                                                                       46 KYNHWFDGLALLHSFTFKNGEVYY - - - RSKYLRSDT -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Last sequence update)
15 JUM 1901 (Rel. 41, Last annotation update)
Myosin Vc (Myosin 5C).
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                                            Pred
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                     73 BB
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Gorry Match
Bost Local Similarity 20...
Acc 90; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  308 -----
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                                                                      60 FTFKNGEVYYRS--KYLRSDTYN-CN--IFANPIVVSEFGTMAYPDPÇKNIFAKAFSYLS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 HTIPEFTDNCLINIMKTGDDYYATSETNFIRKINPQTLETLDKVDY---SKYVAVNL--- 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          622 TTVGSKFRSSLYLLMET----LNATTPHYVRCIKPND----EKLPFEFDSKRIVQQLRAC 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 -----ATSHPHYDSAGNILNMGTSIVDKGRTKYVLFKIPSSVPEKEKKKSCFKHLE 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220 VVCSIPSRSLLQPSYYBSFGITENY·····IVFIEQPFKLDIVK····LATAYIRGVNWA 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       465 ------DKDAEVGSNLVKLPTSATAVKEKDGSIYCQPEILCEGIELPRVNYDYNG 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           562 FLEKNPLTVYDMLVEILRASKFHLCANFEGENPTPPSPFGSMLTVKSAKQVIKFNSKHFR 621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     271 SCLSFHKEDKTWF----HFVDRKTKKE----VSTKFYTDALVLYHHI-----NAYEEDG 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     772 QRKKFLRERRAALIIQOYFRGQQTVRKAITAVALKEAWAAIIIQKHCRGYLVRSLYQLIR 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    317 HVVFDIVAYRDNSLYDMFYLKKL, DKDFEV------NNKLTSIPTCKPFVVPLQY- 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    832 MATITMQAYSRGFLAPRRYRKMIJFEHKAVILQKYAHAWIJARRKFOSI---RRFVLNIOLT 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      889 YRVQRLQKKLEDQNKE-NHGLVEKLTSLAAI PAGDVEKTQKLFAFI EKAATHPPNYEEKG 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSTE: PS50096; 1Q; 4.
Myosin; Repeat, ATP-binding; Calmodulin-binding; Colled coil; Polymorphism.
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Live 73; Mismatches 178; Indels 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.8%; Score 106.5; DB 1; Length 1742;
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                                                                                                                                                                                       Interpro; IPR002710; DIL.
Interpro; IPR001048; IQ_region.
Interpro; IPR001648; IQ_region.
Interpro; IPR001648; IQ_region.
Ptam; PF000612; IQ; 6.
Ptam; PF001843; DIL; 1.
PRINTS; PR00193; MYOSINHEAVY.
PRODOM; PD000755; INFOSINHEAVY.
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                                                                                                                                                                  Genew; HGNC:7604 - MYOSC
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1679
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es 90; Conserv
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DPO2_KLULA

RESULT 12

SIFAIN=GBS 2359 / IFG 1267 / NPRL Y-1140; MEDLINE=88289339; PubMed=3041369; Nucleic Acids Res. 16:5863-5878(1988). Kluyveromyces lactis (Yeast). EMBL; X07776; CAA30603.1; -. 18.68; Conservative TO THE HOST CELL. Plasmid. SONGED. Hest Local Similarity Matches 101; Conserva SEQUENCE FROM N.A. NCBI_TaxID-28985; Plasmid pGK1-2. + {DNA}(N). DNA-binding; PIR: SOUGEO: lactis."; SEQUENCE Query Match NEW TRANSPORT OF COURSE OF THE PRESENCE OF THE PROPERTY OF THE q Ğ qc qq ζč à qq õ d

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-!- MISCELLANDOUS: THE PRESENCE OF THE TWO LINEAR PLASMIDS, IERMED PGKL-1 AND PGKL-2, IN STRAINS OF KLUTVEROMYCES LACTIS CONFERS THE KLIEF PHYNOTYPE, I E PHODUCTION OF TOXIN AND RESISTANCE TO IT, 3.8%; Score 106; DB 1; Length 994; 18.6%; Pred. No. 6.8; IVE 71; Mismatches 160; Indels 212; Caps Townships S., Ricci S., Galsotti C.L.; "Genome organization of the Miller plussid pGML2 from Minymones, es Pukaryota, Pungi, Ascompreta, Saccharomycotina, Saccharomycotes, I.AY I SIMILARITY: BELONGS TO THE DNA POLYMFRASE TYPE B FAMILY. Interpro: IPPONQB64; DNA_POL_B.
Interpro: IPRO04868; DNA_POL_B_2.
Fram: PF03175; DNA_POL_B_2? 1.
SMART: \$800486; POLB6; POLB6; PROSITE; PSO0116; DNA_POLYMERASE_B; 1.
Transferase; DNA-directed DNA polymerase; DNA replication; 994 AA; 117550 MW; 1278F3002D07F1F5 08064; 01-NOV-1988 (Rel. 09, Created) 01-NOV-1988 (Rel. 09, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) DNA polymerase (EC 2.7.7.7) (Plasmid PCKL 2 protein 2). - -GITENYIVFIE- - - - OPPKLDIVKLA Saccharomycetales: Sarcharomycetareae: Kluyveromyces. DPUZ_KIJULA P05468;

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                                                                       728 GEEYFEKDYTENDEI · · · DTLYSMKETHIAUSGEEDPOPLEMWAKIAINSGSYGKEVOR 783
                                                                                                                                             LOEGIELFPVNYLANDKKYKYYAIEVLWSF 428
                                                                                                                                                                                                                                           825 MITEKEDEPIYSIGGISILSASPYPLYKL/KQFF--NIDIIYSOFOSIFVKQKSVLWEL 892
668 TYPVTLLNKHPQEPFNYLNFVPPFINPKFTWEWFKIHEGWYHTYBLIIAKSEGFDIYCHE 727
                                         . SA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                             P70669; P97439,
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sarguence update)
15-JUN 2002 (Rel. 41, Last annotation update)
Metalloendopeptidase homolog PEX (EC 3.4.24.-) (Phosphate regulating neutral endopeptidase) (X-linked hypophosphatemia protein) (HYP)
(Vitamin D-resistant hypophosphatemic rickets protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ecarot B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pex/PEX tissue distribution and evidence for a deletion in the 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  region of the Fex yene in X-link-i hypophosphatemic rice ",
J. Clin. Invest. 99:1200-1209(1997).
-1- FUNCTION: PROBARLY INVOLVED IN BONE AND GENTIN MINEFALIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteloustomi
Mammalia, Eutheila, Rodentia: Sciurognathi, Muridae; Murinae; Mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beck I , Soumounou Y., Martel T , Krishnamurthy G., Gauthier C., Goodyer C G , Tenenhouse H S ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N A MEDLINE-9721775, PubMed-9065736, Strom T.M., Francis F., inster Z.B., Residitioh A., Bovus M.J., Lebrach H., Meitinger T., inster Z.B., Residitioh T.B., Tebrach H., Weitinger T., "Pex jone defortions in Cy and Hyp mice provide mouse medials for X-linked hypophosphatemia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND RENAL PHOSPHATE REABSORPTION.
--- SUBCRELITIAR LACATION: Type II membrane protein (Potential).
--- TISSUE SPECIFICITY. BONE.
--- SIMILARITY FRICONS TO PEPTITASE HAMILY MIR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-96411643, Pubmed-8812412,
Du L., Desbarats M., Viel J., Glorieux F.H., Cawthorn C., Bo
EGRA chouning of the marine Pex yene implicated in X-linked
hypeophosphatcand and evidence for expression in hone.",
Genomics 36:22-28(1996).
                                                                                                                     KIDKDPEVNNYIJSI PTCKPEVVPLQYDKBAR-----VSSNI VKLPT
                                                                                                                                                                                                      TAVKEKDGSIY- - TOPEI .....
                                       310 N-AYEEDGHVVFDIVAYPINSLYDM--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=4724252; PubMed-9977527;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                    429 VPTK 432
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160 YSKYVAVNLATSHPHYDSAGNI----LUMGTSIVDKGRTKYVLFKIPSSVPE-----K 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WMEASS FFRACIEARAY 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   299 -----YIDALVLYHHINAYEELJHVHVEDIVAYEHNSIY------UMFYIPKIPKDFEV 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                345 NNKLESTPFORREVVPLQYEKEAFORSNI VKLEFSATAVKEKEGSTFOQPELLCEGTELP 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.24 -----AVPKTEWFINPTTVNAFYSASINQIPFPAG-----FLQKPFFW------GTEYP 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IV---PIEUPPELLIVELAIAYIROVWASOLSEHFEBRIWERFVERFIRERVOTRF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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N-LIMKED (SICNAC. .) (POTENTIAL).
H LIMKED (SICNAC. .) (POTENTIAL).
N-LIMKED (SICNAC. .) (POTENTIAL).
N-LIMKED (SICNAC. .) (POTENTIAL).
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrolase; Metalloprotease; Zinc; Glycoprotein; Transmembrane;
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BY SIMILARITY.
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ZINC (CATALYTIC) (BY SIMILARITY).
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EXIRACELLULAR (POTENTIAL)
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tive 53, Mismatches 130,
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                                                                                                                                                                                                                                                                                     lnterFig. IPEJOJIW, Peptidase_Ml3.
InterPro: IPPAO(230; Prenyl_site.
                                                                                                                                                                                                                                                                                                                                                                                                                          PPOSITE: PSOU142; ZINC_PPOTEASE; 1
                                                                                                                                                                                                                                                                                                                                          ipponnilan, Za_MTraptdse.
EMBL, 073913, AAC25964 1; EMBL, 073913, AAC25966 1; EMBL, 073914, AAC25966 1; EMBL, 073915, AAC25967 1; EMBL, 075646, AAR47750 1; HSSP, P08473, 1DMT, MROPS, MI3 non
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                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01431; Peptidase_M13; 1.
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749 AA,
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RESULT 14 AROL_PNECA

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                            01-NoV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41), Last annotation update)
16-JUN-2002 (Rel. 41), Last annotation update)
Pent afunctional AROM polypeptide [Includes: 3-dehydroquinate synthase (FC 4.2.1.12) (3-dehydroquinatese); Shikimate 5-dehydroquinatese); Shikimate 5-dehydroquinatese); Shikimate 5-dehydroquinatese); Shikimate 6.2.5.1.13); 3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-enolpyruvylshikimate-3-phosphate synthase) (EPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- CATALYTIC ACTIVITY: 3-deoxy arabino-heptulosonate 7-phosphate = 3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dehydroguinate + phosphate.
-!- CAFALYTIC ACTIVITY: 3-dehydroguinate = 3-dehydroshikimate + H(2)0.
-!- CATALYTIC ACTIVITY: Shikimate + NADP(+) = 5-dehydroshikimate +

    -!- CATALYTIC ACTIVITY: ATP + shikimate = ADP + shikimate 3-phosphate.

                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota: Pungi: Ascomycota: Pneumocystidomycetes, Pneumocystidaceae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate = phosphate + 5-0-(1-carboxyviny1)-3-phosphoshikimate.
-i- PATHWAY: SECOND TO SIXTH STEPS IN THE BIOSYNTHESIS OF CHORISMATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Gen. Microbiol. 139:2901-2914(1993).
-!- FUNCTION: THE AROM POLYPEPTIDE CATALYSES 5 CONSECUTIVE ENZYMATIC
REACTIONS IN PRECHOPISMATE POLYAROMATIC AMING ACTER REGSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE SHIKIMATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :!- SIMILARITY: IN THE 3RD SECTION; BELONGS TO THE SHIKIMATE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The cloning and characterization of the arom gene of Pheumocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WITHIN THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Banerji S., Waketield A.E., Allen A.G., Maskell D.J., Peters S.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- SIMILARITY- IN THE N-TPPMINAL SECTION; BELONGS TO THE DEHYDROQUINATE SYNTHASF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Atomatic amino acid biosynthesis; Multifunctional enzyme;
   PRT 1581 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000623; Shik_kinase. Plane: Province Pro; IPR002907; Shik_kinase. Plane: Province Provinc
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Probom: PD001867; EPSP_syntase; 1.
TIGPFAMS: TIGPF01093; arob; 1.
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InterPro; IPRO01381; DHquinase_I.
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PF01488; Shikimate_DH; 1.
PF01761; DHQ_synthase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Piam; PF00275; EPSP_syntase; 1.
                                                                01-NOV-1997 (Rel. 35, Created)
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   STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                            Pneumocystis carinii.
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AROL PNECA
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959 LLISYLEANSIVIHIHENIQTIIKYLNIFKTPAPYQUNIMHVWFPPKPWY----NLYSS 1013
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                                                                                                                                                                                                                                                                                        56 ILHSFTFKNGFV--YYRS-----KYLRSDTYNCNIEANRIVVSEFGTMAYPDFWKNIFAK 108
                                                                                                                                                                                                                                                                                                                                                        109 AFSYLSHITP-FFIDNCLINIMKIGDOYYAISETNEIRKIDPQILELLDAVDYSKYVAVN 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         270 ASCLSPHKEDKTWFHFVD-----RKTKKEVSTKF-YTDALVLYHH------IN 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            357 RFVVPLQYDK-DAFVGSNLVKLPTSATA-----VKEKDGSIYCQPEILCEGIELPRVNY 409
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-!- FUNCTION: ACTS WITH KNA POLYMEKASE TO INITIALE TRANSCRIPTION FROM
EARLY GENE PROMOTERS. A DNA-BEPENDENT AIPASE ACTIVITY IS
                                                                                                                                                                                                                                                                                                                                                                                                                        158 LAISHPHYISAGNILNMGTSIVIRGPIRKYNLFEITSSVFEKERKKSGTEHLEVVGSITSP
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Melanoplus sanquinipes entomopoxvirus (MSEPV).
Viruses; dsDNA viruses, no ENA stage; Poxviridae; Entomopoxvirinae:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Atonso C.L., Tulman E.K., La Z., Gma E., Kutlish G.F., Fock D.L., "The genome of Melanoplus sanguinipes entomopoxyirus.":
                                                                                                                                                                                                                                                      76; Mismatches 160; Indels 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            le-OCT-2001 (Rel. 40, Created)
16 OCT-2001 (Rel. 40, Lust sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Barly transcription factor 70 kba subunit (VETF small subunit).
 Transferase; Finase; NADP; ATP-binding.
                                                                                                                                                   1217 1217 FORMS A SCHIFF-BASE INTERMEDIATE (BY SIMILARITY).
1581 AA; 178043 MW; 417A8435b061170F CRC64;
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               3-DEHYDROQUINATE SYNTHASE.
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                                                                                   SHIKIMATE DEHYDROGENASE.
                                                 SHIKIMATE KINASE
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ACT_SITE
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This SWISS-PROT carry is copyright. It is produced through a collaboration between the SWIss fustfute of Bioinformatics and the EMEM, outstation the European Bioinformatics institute. There are no issue by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial cultilies iequires a license agreement (see http://www.isb-sib.ch/aunounce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 SIMDIWISKLYDSLLLLNKNDKYNLNNIEFTTKSR-LNEELLGTNKNINDIITENIKKYD 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 GTMAYPDPCKNIFAKAFSYLSHTIPEFTDNCLINIMKTGDDYY----ATSETNFIRKI-D 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 NYIIIIDEAHNFFGNASGEL------LIHIKONSTARYVELTGSPISNTIESEKD 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149 PQTLETLDKVDYSKYVAVNLATSHPHYDSAGN-----ILNMGTSIVDKGRTKYVLF--- 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200 ---KIPSSVPEKEKKKSCFKHLEVVCSIPSRSLLQPSYYHSFGITENYIVFIEQPFKLDI 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235 DRKEIPSPIFGGNIK--LLNYPVVLC--PMSKLQEDNYNMISNOTEN-DMFIKLMMNVSL 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       257 VKLATAYIRGVNWASCLSFHKEDKTWFHFVDRKTKKEVSTKFYTDALVLYHHINAYEEDG 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 IIGDIKYNHWFDGLALLH --- SFTFKNGEVYYRSKYLRSDTYNCNIEANRIVVSEF --- 93
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Pran; PPC0176; SNF2_N; 1.
PROSITE; PS00690; DEAH_ATP_HELICASE; FALSE_NEG.
Helicase: Transcription regalation: Activator; ATP-binding.
NP_BIND 45 52 ATP (POTENTIAL).
NP_BIND 45 52 DENH BOX.
-!- SUBLUNIT. HETFPONIMEP OF A 70 KDA AND A 82 KDA SUBUNIT.
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Search completed: July 15, 2003, 69:28:08 Job time : 27 secs

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OM protein - protein search, using sw model

July 15, 2003, 09.26.34; Search time 27 Seconds (Without alignments) 573.202 Million cell updates/sec Run on:

US-10-053-192-1 2825

MHLDLHGMFIPONDLGAETE 526 1 METIFNPNKEEHPEPIKAEV Title: Perfect score. Sequence:

Scoring table:

BLOSUM62 Gapop 10 0 , Gapext 0.5

262574 Total number of hits satisfying chosen parameters:

262574 seqs, 29422922 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 100% Maximum Match 100% Listing first 45 summaries

Issued_Patents_AA:* Database :

1. /cgg2_6/ptrodata/l/iaa/5A_commupep.*
2. /cgn2_6/ptrodata/l/iaa/5H_commupep.*
3. /cgn2_6/ptrodata/l/iaa/5A_commupep.*
4. /cgn2_6/ptrodata/l/iaa/6A_commupep.*
5. /cgu2_6/ptrodata/l/iaa/ptrlUS_COMMupep.*
6. /cgn2_6/ptrodata/l/iaa/ptrlUS_COMMupep.*
6. /cgn2_6/ptrodata/l/iaa/parkfiles! pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query	Query Match Length	DB	qI	Description
1	1071	37.9	533	4	US-09-385-259-2	Sequence 2, Appli
2	1071	37 9	533	4	US-09-645-370-2	ci
3	1070	37.9	533		11S-08-488-305A-6	·c
4	373.5	13.2	205	4	US-09-385-259-3	'n
5	373.5	13.2	205	4	US-09-645-370-3	3
9	108.5	3.8	3224	C a	US · 08 · 705 · 660 · 34	34,
7	108.5	3.8	3224	e	US-08-989-045-34	34,
8	106	3.8	663	4	115-09-134-078-61	61,
6	106	α «·	680	4	115-114-1 44-0 78-25	25,
10	100.5	3.6	503	4	US-09-134-001C-2996	2996
11	100	ر. د.	1568	7	US-00-181-706-2	C i
12	100	3.5	1568	4	US-09-458-791-2	Sequence 2, Appli
13	100	3.5	1568	4	US-09-454-056-2	٠;
14	86	3.5	984		US-08-257-073-3	3,
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17	86	3.5	984	₹	US-08-460-736-120	120,
18	86	3.5	686	4	US-08-213-419B-2	2, A
19	86	3.5	989	❖	US-08-213-419R-4	Sequence 4, Appli
20	97.5	3.5	574	4	US-09-134-001C-3141	31
21	96.5	7	2391	C 1	TIS-08-446-855A-2	Segmence 2, Appli
22	96 S	4	2341	4	TS-09-150-741 2	ci
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56	46	3.3	724	۱,	US-09-121-964 1	i
27	93.5	. 3 . 3	831	4	US-09-269-861A 8	α

Sequence 10,	sequence 13,	Sequence 13,		Sequence 30,	Sequence 13,	Patent No.			Sequence	Sequence 1, 1	Sequence	Sequence 5, 1	Sequence	Sequence 14,	Sequence 3,		Sequence 8, Appl
(1) - 0365-401-50-50	118-08-04-04-8U-31	. ns-nu-170-996-13	US-08-609-049A-30	US-09-1/0-996-30	US-09-251-645-13	, 5194600-4	TIS-08-836-687B-	US UB 961 083-20	1 021 197 80-20 1	US-09-132-271-1	US-U9-142 334 22	. US-U8-160-676A-5	11S-08 141-324-14	US-08-541-902-14	US-09-180-439-3	0.15-09-180-439-4	TIS-09-180-439-8
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ALIGNMENTS

UT 1 19-385-259-2 quence 2, Application tent No. 620114 NREPAI INFORMATION. PPLICANT: Acland, Gr PPLICANT: Bay, Kunal LILE OF INVENTION. II TILE OF INVENTION. II TILE OF INVENTION. II THE OF INVENTION. III THE OF INVENTION. II THE OF INVENTION. II THE OF INVENTION. III THE OF INVENTION. II THE OF INVENTION. II THE OF INVENTION. III THE OF INVENTION. II THE OF INVENTION. II THE OF INVENTION. III THE OF INVENTION. II THE OF INVENTION. II THE OF INVENTION. III THE OF INVENTION. II THE OF INVENTION. II THE OF INVENTION. III THE OF INVENTION. II THE OF INVENTION. II THE OF INVENTION. III THE OF INVENTION. II THE OF INVENTION. II THE OF INVENTION. III THE OF INVENTION. II THE OF INVENTION. II THE OF INVENTION. III THE OF INVENTION. II THE O	TIS/UB4R4259 DISTAND D. SOLY M. DENTIFICATION OF CONSENTIAL STATIONARY NIGHT BELNIGHESS N DOGS N DO	37.9%; Score 1071; DB 4; Length 533; 42.2%; Fred. Nc. 1.5e-99; 11ive 92; Mismatches 188; Indels 24; Gaps 12;	2 ETIFNRNKEEHPEPIKAEVOGQLPTWLQGVLLRNCPGMHTIGDTKYNHWFYGLALLHSFT 61	FKNGEVYYRSKYLRSDTYNCNIEANPIVVSEFGIMAYPDPGKNIFAKAFSYLSHIIPEFT 121 	PROLINIMKTGDUYYATSELNFIEKIBEGTLETLEKULYSKYVAVALATSHPHYBSAGNI 181 - - - - - - - - - - - - - - - - - -	182 LAMOUSIVEGETZYVLPY (PSSVEEZPYA SOTA OLEVVOSTESESLI QUSYYBSFGIT 241 	242 ENYIVETEOPEKLITYKLATAY (PGVAMASC) STHEFOVTWHITVESPYTREVSTRIYT 309 24.2 ENYIVEVSTIVESMLLESSWSIMSAHYM, SELSH IMOVH GALFEEFFF HURYPT 306
рофикатын тирин с рфф	PESULT 1 US-09-385-259-2 US-09-385-259-2 US-09-385-259-2 Patent NO. 6201114 PAPPLICANT: Aguirre, Gustavo D. APPLICANT: Aguirre, Gustavo D. APPLICANT: Acland, Gregory M. APPLICANT: Pay. Kunal IIILE -F INVENTION: IN DOGS FILE PEFFENNY: 1940-42481 CUFFENY TELLO TO NEMHER: 05/03/219 CUFFENY TELLO TELLO NOMBER: 60/103,219 EARLIER APPLICATION NUMBER: 60/103,219 EARLIER APPLICATION NUMBER: 60/103,219 EARLIER APPLICATION NUMBER: 60/103,219 EARLIER APPLICATION NUMBER: 60/103,219 SOFTWARE: PALENT DATE: 1948-10-06 NUMBER OF SEQ ID NOS: 8 SEQ ID NO 2 LENGTH: 533 TYPE: PRI TELLO TO	Query Match 37.9%; Score 1071; DB 4; Best Local Similarity 42.2%; Fred. No. 1.5e-99; Matches 222; Conservative 92; Mismatches 188;	2 ETIFNRNKEEHPEPIKAEVOC 			182 LAMGISINLEGERIKYNLER H 	242 ENYIVFIEOFFKLLTVKLATA 1 1 1 1 1 1 1 1 1 1

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APPLICANT AGUITCE, GUSTAVO D.
APPLICANT ACLAND, Gregory M.
APPLICANT ACLAND, Gregory M.
APPLICANT RAY, KANDA
TITLE OF INVENTION: IDENTIFICATION OF CONGENITAL STATIONARY NIGHT BLINDNESS
TITLE OF INVENTION: 10 DOGS
TITLE OF INVENTION OF TOTAL O
357 REVVPLQYDKDAEVGSNLVKLP-TSATAVKEKDGSIYCQPEILCEG----IELPRVNYD- 410 | 1:11 | 1 | 1:1 | 1 | 1:1 | 1 | 1:1 | 367 RSVLPLNIDK-ADTGKNLVTLPNTTATATI.RSDETIMLEPEVLFSGPRQAFEFPQINYQK 425
                                                                                                                                                                                         411 YNGKKYKYVYATEVQWSPVPTKIAKLNVQTKEVLHWGEDHCWPSEPIFVPSPDAREEDEG 470
                                                                                                                                                                                                                                                                                 426 YGGKPYTYAYGLGLNHF-VPDRLCKENVKTKETWVWQEPDSYPSEPIFVSHPDALBEDDG 484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           307 SSPNLFHHINTYEDNEPLIVDLCCWKGFEFVYNYLYLANIRENWEFVKKNARKAPQPEVR 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 411 YNSKAYKYVYATEVQMSEVETKIAKIANGETKEVLHMSEDHCWPSEPIFVPSPDAREEDEG 470
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                                                                                                                                                                                                                                                                                                                                                                              471 VVLTCVVVSEPNKAP-FILIIDAKTFKELGRATVNVEMHLDLHGMF 515
                                                                                                                                                                                                                                                                                                                                                                                                                              : Sequence 2, Application US/09645370
: Patent No. 6428958
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ORGANISM: Canis familiaris
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Matches 222, Conservative
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                                                                                                                                                                                                                                             APPLICANT: B vik, Claes Olof, Briksson, Ult; Peterson, Per A. TITLE OF INVENTION: isolated Protein Receptors, Antibodies Which TITLE OF INVENTION: bind Thereto, Nucleic Acid Sequence Coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.9%; Score 1070; DB 1; Length 513; 42.0%; Pred. No. 1.9e-99;
                                      471 VVLTCVVVSEPNKAP-FLLILDAKTFKELGRATVNVEMHLDLHGMF 515
                                                            92; Mismatches 189, Indels
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MEDIUM TYPE: Diskette, 3.5 inch, 1.44 kb storage
                                                                                                                                                                                                                                                                                                       Patent No. 5679772
TITLE OF INVENTION: Therefor, And Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: LUD 5280.3
TELECOMMUNICATION INFORMATION:
TELEFNORE: (212) 688 9200
TELEFAX. (212) 838-3884
INFORMATION FOR SEQ 1D NO: 6:
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                                                                                                                                                                            Sequence 6, Application US/08488305A Patent No. 5679772
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NAME: Kohli, Vincet
REGISTRATION NUMBER: 37,003
                                                                                                                                                                                                                                                                                                                                                                                         SEE: Felfe & Lynch
: 805 Third Avenue
New York City
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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APPLICANT: Aguirre, Gustavo D.
APPLICANT: Acland, Gregory M.
APPLICANT: Ray, Kunal
TITLE OF INVENTION: IDENTIFICATION OF CONSENITAL STATIONARY NIGHT BLINDNESS
TITLE OF INVENTION: IN DOGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ray, Kunal TITLE OF INVENTION: IDENTIFICATION OF CONGENITAL STATICNARY NIGHT BLINUNESS TITLE OF INVENTION: IN DOGS
307 SPENLEHHINTYEDHEFLIYDLOOWKGEBFYYNYLYLAN FENWEEVKKNAKKAE'2'EE'F 3 55
                                                                                                  411 YNGKKYKYVYATEVQWSPVPTKIAKLNVQTKEVLHWGEDHCWPSEPIFVPSPDAREEDEG 470
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                                                                                                                                                                                                                                                                       471 VVLTCVVVSEPNKAP-FLLILDAKTFKELGRATVNVEMHLDLHGMF 515
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CURRENT PAPELCATION NUMBER P. 18/09/645, 370
CURPENT FILING DATE: 2020.08.24
PRIOR FILING DATE: 1099-08-30
FRIOR FILING DATE: 1999-08-30
FRIOR PAPELCATION NUMBER: 60/103,219
FRIOR FILING DATE: 1998-10-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 19603/2481
CURRENT APPLICATION NUMBER: US/05/385,259
CURRENT FILING DATE: 1999-08-30
EARLIER APPLICATION NUMBER: 60/103,219
EARLIER FILING DATE: 1998-10-35
NUMBER OF SEQ ID NOS: 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 3, Application ທະ/ກີຈີ;ຂາງສຸງ
; Patent No. 6201114
; GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 3, Application US/09645370 ; Patent No. 6428958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Aguirre, Gustavo D. APPLICANT: Acland, Gregory M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWAPE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
US-09-385-259-3
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72 PKESHVTYHPBP1955AYVPAMTEFP1VTEP577*APFFFFFFFFFFFFFFFF7V - FVT 129
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                                                                                                                                                                                                                                                                                                         62 PRNGEVYYPSKYLPSDTYNGNIEANPIVVSFPGTMAYPDPCKNIFAKAFSYLSHTIPEFT 121
                                                                                                                                                                                                                               2 ETIFNRNKEEHPEPIKAEVQGQLPTWLQGVLLRNGPGMHTIGDTKYNHWFDGLALLHSFT 61
                                                                                                                                                                                                                                                                    17 ETV-----EELSSPLTAHVTGRIPLWLTGSLLRCGPGLFEVGSEPFYHLFDGQALLHKFD 71
                                                                                                                                                                                        7; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.8%, spore 108.5, DB 2, Lenath 3224; 22.1%, Pred. No. 9.7,
                                                                                                                                             13.2%, Score 373.5, DB 4; Length 205; 49.3%; Pred. No. 1.18-29; tive 21; Mismatches 46; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INCOPMATION:
APPLICANT: KEESEE, SUSAN
APPLICANT: CBAR, ROBERT
APPLICANT: WWW, YING-JYE
TITLE OF INVENTION: METHORS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: DETECTION OF CHRUICAL CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patentin Pelease #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267 VNWASCL-----SPHKEDKTWFHFVDRKT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MTP-023 (8395/27)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E. Testa, Hurwitz & Thibeault.
125 High St.
                                                                                                                                                                                                                                                                                                                                                                                                            122 DNCLINIMKIGDEYYATSETNFIRKI 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 44, Application US/UB/USA60
Patent No. 5858683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: GREENHALGH, DUNCAN A REGISTRATION NUMBER: 38,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (61?) 24½-7660
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 34:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3224 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                      72; Conservative
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                                                                                          OFGANISM: Canis familiaris
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MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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CLASSIFICATION: 424
NUMBER OF SEQ ID NOS: 8
                Patentin Ver
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                                                                                                                                                 Guery Match
Best Local Similarity
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Bost Local Similarity
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                                                     LENGIH: 205
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                SOFTWAPE F
                                                                         TYPE: PRT
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ADDRESSEE: Gray Cary Ware & Freidenrich LLP STREET: 4365 Executive Drive, Suite 1600
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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pre- nanin/n24ng2
                                                                                                                                                                                                                                                                                                                                                                                                                              GLYCOSIDASE ENZYMES 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/134,078
FILING DATE: 13-AUG-1998
CLASSIFICATION: 435
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APPLICATION NUMBER: 08/949,026
FILING DATE: 10-0CT-1997
APPLICATION NUMBER: 62/056,916
FILING DATE: 06-DEC-1996
AILORNEY/AGENI INFORMATION:
                                                                                                                                                                                                                                                                                                                                         Sequence 61, Application US/09134078 Patent No. 6368844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER OF
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bylina, Edward J.
TITLE OF INVENTION: GLYCOSID
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
                                                                                                                         390 SIYCOPEILCEG-----
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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amino acid
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haile, Lisa A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
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Best Local Similarity
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                                                                              339 LDKDFEVNNKLF--SIPTCKR-----FVVPLQYDKDAEVGSNLVKLPTSAFAVKEKDG 389
                                                                                                                                                                                                                      390 SIYCQPEII.CEG-----IELPR----VNYDYN-GKKYKYVYATEVQWSPVP 430
                 576 VHWAEGLOKTGSGLNSFYLOPET ----YTGRSVHYWKKVLPLLKTTKKKNSTPEPTDPLFK 631
                                                           692 --EDIE-NDALSPEEGEEGKNYLRKTRDYLIKIIDDSDSNL-SVVKKLPVPLESVKEMLN 747
                                                                                                                                                                                                                                                             748 SVMQELEDYSEGGPLYKNGSLRNADSETKRSTPSPTRYSLSPSKSYKYSPKTPPRWAEDQ 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267 VNWASCL-----SFHKEDKTWFHFVDRKT------KKEVSTKFYTDALVL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   576 VHWAECLOKTGSGLNSFYDQRE----YIGRSVHYWKKVLPLLKIIKKKNSIPEPIDPLFK 631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.8%; Score 108.5; DB 3; Length 3.24; Prest Local Similarity 22.1%, Fred. No. 6.7,
                                                                                                                                                                                                                                                                                                     431 TKIAKLNVQTKEVL------HWGEDHCWPSE---PIFVP 460
                                                                                                                                                                                                                                                                                                                                 808 NSLLKMICGGVEAIKKEMQELKINSSNSASPHRWPTENYCPOSVP 852
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                METHODS AND COMPOSITIONS FOR THE DETECTION OF CEPVICAL CANCER
                                                         306 YHH-----INAYEEDGHVVFDIVAYEDNSLYD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/589,045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86;
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REGISTRATION NUMBER: 38,678
REFERENCE/DOCKET NUMBER: MTP-023 (8395/27)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: KEESEE, SUSAN
APPLICANT: CBAR, ROBERT
APPLICANT: OBAR, ROBERT
APPLICANT: OBAR, ROBERT
TITLE OF INVENTION: METHODS AND COMPOSITIO
TITLE OF INVENTION: NETECTION OF CEPVICAL.
NUMBER OF SEQUENCES: 46
COPPESPONDENCE ADDRESS:
COPPESPONDENCE ADDRESS:
STREET: 125 High St.
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Patent No. 6027905
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
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632 HFHSVDIQASEIVEYEEDAHITFAILDAVNGNIEDAVTAFESIKSVVSYWNLALIFHKKA 691
                                                                                                                  339 LDKDFEVNNKLT--SIPICKR-----FVVPLQYDKDAEVGSNLVKLPTSATAVKEKIG 489
                                                                                                                                                                                                                                     692 --EDIE-NDALSPFEGEEGKNYLPKTPDYLIKIIDDSDSNL-SVVKKLPVPLESVKEMLN 747
                                                                                                                                                                                                                                                                                                                                                       -----IELPR----VNYDYN-GKKYKYVYAIEVQWSPVP-430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    748 SVMGELELYSEGGPLYKNGSLENALSEIKRSTPSPTRYSLSPSKSYKYSPKTPPRWAEDU 807
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21.4%; Pred. No. 0.09;
2.ve 65; Mismatches 210; Indels 214; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                431 TKIAKLNVQTKEVL-------HWGEDHCWPSE---PIFVP 460
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....weifi. 680 amino acids TYPE: amino acid TYPE: Ilori Olectrical

MOLECULE TYPE: protein FRAGMENT TYPE: internal

SEQUENCE CHARACTERISTICS:

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275 YPSHWGVSPENYAQWGAKWIED-----HIKIAKEIGKPVVLEEYGIPKSAPVNRTAIYR 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 502 ----SPEEVKNWWNSGTWQAE---FGSPDIEWNGEVGNGALQLNVKLPGKSDWEEVRVA 553
                                                            175 YDS----AGNILNMGTSIVDKGRTKYVLFKIPSSVPEKEKKKSGFKHLEVVCSTPSPS) I. 230
                                                                                                     180 REEPTIMAWELANEPRCETDKSGNTLV-----EWVKEMSSY----IKS--L 219
                                                                                                                                             231 QPSYYHSF---GITENYIVFIEQPFKLDIVKLATAY--IRGVNWASCLSFHKEDKTWFHF 285
                                                                                                                                                                                      220 DPNHLVAVGDEGFFSNY----EBPRPYGGEAEWAYNSWSGVDWKKLLSIETVDEGTFHL 274
                                                                                                                                                                                                                              286 -----VDRKTKKEVSTKFYTDALVLYHHINAYEEDGH-VVFD------IVAYR 326
                                                                                                                                                                                                                                                                                                                      ----KLT 350
                                                                                                                                                                                                                                                                                                                                                       329 IMNDLVYDIGGDGAMFWMLAGIGEGSDRDERGYYPDYDGFRIVNDDSPEAELIREYAKLF 388
                                                                                                                                                                                                                                                                                                                                                                                                    351 SI-----PICKREVVP---LQYDKDAEVGSNLVKLPIS--ATAVKEKDGSIYCQPEILC 399
                                                                                                                                                                                                                                                                                                                                                                                                                                             389 NTGEDIREDICS-FILPKDGMEIKKTVEVRAGVFDYSNTFEKLSVKVEDLVFENEIEHLG 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        400 EGI-----ELPRVNYD----YNGKKYK------YVYATEVQWSPVPTKI 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             434 AKLNVQTKEVLHWGEDHCWPSEPIFVPSPDAREEDE-GVVLTCVVVSEPNKAPFLLILDA 492
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                                                                                                                                                                                                                                                                                                                 327 -- DNSLYD------ MFYL-----KKLDKD-------FEVNN----
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SOFTWARF: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: GLYDOSTHASF ENZYMES
NUMBER OF SEQUENCES: 72
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UMBER: US/09/134,078
13-AUG-1998
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Patent No. 6368844
GENERAL INFORMATION:
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FILING DATE: 10-0CT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 10-0CT-1997
APPLICATION NUMBER: 60/056,916
FILING DATF: 06-DEC-1996
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACTO SEQUENCES FELALING TO STAPHYLOCOCC
TITLE OF INVENTION: EPIDEPMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                              146 WDDFGGMNOYVPWFGGTHHDDFYPDEKI------KEEYKKYVSFLVNHVNTYTGVPY 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175 YDS----AGNILNMGTSIVDKGRTKYVLFKIPSSVPEKEKKKSCFKHLFVVCSIPSKSLL 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197 REEPTIMAWELANEPPCETDKSGNTLV------EWVKEMSSY-----IKS---L 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     231 @PSYYHSF---GTIENYIVFIE@PFKLDIVKLATAY--IPGVNWASTISFHKERYTWEHF 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  286 ------VERKIKKEVSIKEYIDALVLYHHINAYEEDSH-VVFD--------TVAYP 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     292 YPSHWGVSPENYAQWGAKWIED-----HIKIAKEIGKPVVLEEYGIPKSAPVNRTAIYR 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---KI.T 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              351 SI-----PTCKRFVVP---LQYDKDAEVGSNLVKLPTS--ATAVKEKDGSIYCQPE1LC 399
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                                                                                                                                                                                                                                                                           75 ESDIYNGNIEANRIVVSEFGIMAFPDFCKNIFAKAFSYLSHT! FEFTDNGLIMIMKI 131
                                                                                                                                                                                                                                                                                                                                                                                         132 CPD------YYATSETNFIF--KIPPQTLETLDKVPYSKYVA-----VNLATSHPH 174
                                                                                                                                                                                                 40 GKFAINGKEFPFIGSNNYYMHYKSWGMIDSVLESAPDMGIKVI.PIWGFI475ESYCPDK-- 97
                                                                                                                                                                30 GVLLRNGPGMHTIGETKY-----NHWFD------GLALLHSFTFKNGEVYYRSKYL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             237 DPNHLVAVGDEGFFSNY----EGFKPYGGEAEWAYNGWSGVDWKKLLSIETVDFGTFHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  465 YGIYGFDLDTTRIPDGEHEMFLEGHFQGKTVKDSIKAKVVNEARYVLAEEVDFS-----
                                                                                                       65; Mismatches 210; Indels 214; Gaps
                                                  3 88; Soor 106; DB 4; Length 680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                327 -- DNSLYD-----FFYL-----KKLDKD------FEVNN--
                                                                                Pred No u.u94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PPLOP APPLICATION NUMBER: US 60/064,964 PPLOP FILING NATE: 1997-11-08 PPLOP APPLICATION NUMBER: US 60/055,779 PPLOP FILING NATE: 1997-08-14
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Patent No. 6380370
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                                                                                21 48:
                                                                                                       Matches 133; Conservative
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                                                                                Rest Local Similarity
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US-09-134-078-25
                                                     Query Match
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66 EVYYRSKYLRSDIYNCNIEANRIVVSEFGTMAYPDPCKNIFAK---AFSYLSHT---IPE 119
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                                                                                                                                                                                                                                                                                                                                                                                        114 LSNETIDGGVDALDVLESTTLDTYFTEFLTTINKTTDFAKKIANNTIKQIRENIELKKAN 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          206 PEKE-----KKKSCFKHLEVVCSIPSR-----SLLQPSYYHSFGITENY 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          245 IVFTEQPFKLDIVKLATAYIRGVNWASCI.SFHKEDKTWFHFV-DRKTKKEVSTKFYTDAL 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       304 V-LYHHINAYEEDGHVVFDIVAYRDNSLYDMFYLKKLDKDFEVNNKLTSIPTCKRFVVPL 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      331 IESONTINEEMKKODLISONELYYLTTIEDTFHFALFTAISDLMDELVLV-TSKIIQSAT 389
                                                                                                                                                                                                  Gaps
                                                                                                                                         3.6%; Score 100.5; DR 4; Length 509;
20.1%; Pred, No. 0.21;
Live 69; Mismatches 130; Indels 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: --to be assigned-- (USSN 08/958,598 APPLICATION NUMBER: conversion to Provisional application)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Melanie K. Spriggs, Michael R. Comeau, APPLICANT: Mobert F. DuBose, Richard S. Johnson FITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/958,598 (converted to a APPLICATION NUMBER: Provisional, see below)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn Release #1.0, Version #1.30
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                                                                      ORGANISM: Staphylococcus epidermidis
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Patent No. 6130068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                                                                                                              Hest Local Similarity 20.1%
Matches 73; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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                                                                                          US-09-134-001C-2996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
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SEQ 1D NO 2996
LENGTH: 509
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                                                 TYPE: PRT
                                                                                                                                            Query Match
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122 DNCLINIMKT-----GDDYYATSETNFIRKIDPQTLETLDKVDYSKYVAVNLATS 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 HPHYDSAGNI--LUMGTSIVDKG--RTKYVL-----FKIPSSVPEKEKKESCPKHLEVV 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222 CS-----IPSRSLLQPS-----YYHSFGITENYIVFIEQFFKLDIVKLA 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                261 TAYIRGVNWASCLSFHKEDKTWFHFVDRKTKKEVSTKFYTDALVLYHHINAYEFEIXHVVF 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                321 ELVAYPENSEYEMFYEKLEKEEPVNIKLESTIFFERFVVFLANTIAFFASSNIVKLETS 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       381 ATAVKEKDGSIYGQPEILGEGIELPRVNYLYNDSRAYRYVYAFRUWNSPVFFRIANI,NVQF 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                  3.5%; Score 100; DB 4; Length 1568; 19.6%; Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                     19.6%; Pred. No. 1.5;
tive 58; Mismatches 137; Indels
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RECEPTOR DNA AND POLYPEPTIDES
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-10/8/Windows 95
SOFTWARE: Word for Windows 95, 7.0a
CURRENT APPLICATION DATA:
                                                                                                          REFERENCE/DOCKET NUMBER: 2631-A TELECOMMUNICATION:
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STREET: 51 University St.
Outober 26, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/69458791
Patent No. 6174689
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TITLE OF INVENTION: VIPAL FN
                                                                                         34,347
                                                                                                                                                       TELEFHONE: (206)470-4189
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 2:
                                          ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                LENGTH: 1568 amino acids
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Matches 71; Conservative
                                                                  NAME: Henry, Janis C
REGISTRATION NUMBER;
                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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                         CLASSIFICATION:
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FILING DATE:
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APPLICATION NUMBER - US/69/458,791

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222 CS-----IPSRSLLQPS-----YYHSFGITENYIVFIEQFFKLDIVKLA 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              381 ATAVKEKDGSIYCQPEILCEGIELPRVNYDYNGKKYKYVYATEVOWSPVPTKIAKLNVQT 440
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IIILE OF INVENTION: VIRAL ENPODED SEMAPHORIN PROTEIN
IIILE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/958,598
FILING DATE: 28-0C7-1997
ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE: protein
SFQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                           NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
PEFEBENCE/POCKET NUMBER: 2631
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                      TELEPHONE: (206)470-4189
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 2
FILING DATE: 10-Der-1999
                    CLASSIFICATION - Unknown
                                                                                                                                                                                                                                                                                                                                           LENGTH: 1569 amino acids
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Patent No. 6187909
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IRM PC compatible
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51 University St
                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71; Consorvative
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-458-791-2
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321 DIVAYRDNSLYDMFYLKKLDKDFEVNNKLTSIPTCKRFVVPLQYDKDAEVGSNLVKLPTS 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       632 EDDPVAVEKISGGGRPKENKONRINGALDVFYIKSIEPDKVSILGK-----SNVIVT 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            684 GANFTRASNITMILKCISTCDKDVIQVSHVLNDTHMKFSLPSS--RKEMKNVCIQFDGGN 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 222 CS-----IPSRSILQFS----YYHSFGITENYIVFIEQFFKLDIVKLA 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261 TAYIRGVNWASCLSFHKEDKTWFHFVDRKTKKEVSTKFYTDALVLYHHINAYEEFGHVVF 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      802 VA------IYOGFLAPSIK---SSKVFINVIVKLFVGDTYLDCG---- 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 ATAVKEKPGSIYCQPEILCEGIELPRVNYPYNGKKYKYVYATFVQWSPVPTKIAKLNVQT 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 879 ILLEHGENSQLNISEENIIPNQUITTIICKIKGIKIASTIANSSA AVEVNIGNLEDAV 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 HPHYDSACNI--LNMGTSIVDKG--RTKYVL-----FKIPSSVPEKEKKKSCFKHLEVV 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   742 CSSVGSLSYIALPHCSLIFPATTWISGGQNITMMGPNFPVIDNI,IISHELKGNINVSEYC 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           837 - TLGYPEDPPTGYPVFS-----FVFTF1 F-----VK19KEND---NFN1SKKD1E-878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 3.5%, Score 100; DB 4; Length 156%;
Best Local Similarity 19.6%, Prod. No. 1.5;
Matches 71, Conservative 58, Mismatches 177, Indels 96; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE NUMBER OF SPRUENCES: 143
CORPESPONDENCE ADORESS:
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OPEPATING SYSTEM: MS-POS/Windows 95
SCHWARE. Wild El Windows 55, 7,0a
CURRENT APPLICATION DATA.
APPLICATION NUMBER: IIS/09/459,066
                                                                                                                                                                                     08/958,598
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Patent No. 5766597
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APPLICANT: de Taisne, Charles
APPLICANT: Tine, John A.
                                                                                                                                                                                                                                                               NAME: Henry, Janis C
REGIETRATION NUMBER: 34,347
PEPEFENCE/COCKET NYMBEP: 26
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                  (206)470-4189
                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGIH: 1568 amino acids
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                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                     APPLICATION NUMBER:
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STATE: New York
COUNTRY: UNITED
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                                                                                                                                    CLASSIFICATION:
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                                                                                                              FILING DATE:
                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
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UNITED STATES OF AMERICA

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125 LINIMKTGDDY - - YATSETNFIR-KIDPQTLETLD - - KVDYSKYVAVNLATSHPHYDS 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 FGI----TENYIVFIEQPFKIDIVKLATAYIPG-VNWASGISFHKEDKTWFHFVDPKTKK 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       305 NGTNLIESKNYALGSDIPEKCITI, ASNOFTSGNFNIEKCE OCAL ---LVEKENKN 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     335 -----YLKKLD----KDFEVNNKLTSIPTCKRFVVPLQYDKDAEVGS 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         374 NLVKLPTSATAVKEKDGSTYCQPETICFGIELPRVNYD------YNGK 414
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Matches 67; Conservative 49; Mismatcher
                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1 30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 454310-2570 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA.
APPLICATION NUMBER: US 07/852,305
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                       APPLICATION NUMBER: US/08/257,073
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                             US 07/672,183
ZIF. 16036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPRATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5843975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Frommer, William S. REGISTRATION NUMBER: 25,506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEX: 42506 CURTMS
INFORMATION FOR SEQ 1D NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07 FILING DATE: 20-MAR-1991 ATTORNEY/AGENT INFORMATION:
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APPLICANT: Paoletti, Enzo
APPLICANT: Tartaqlia, James
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125 LINIMKIGDDY----YATSETNPIR-KIDPQJI,ETLD--KVDYSKYVAVNLA1SHPHYDS 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 AGNILUMGISIVINKGPIKYVLFKIPSSVPEKERKKSCFKHLEVVCSIPSPSLLQPSYYHS 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  305 INCLULESKNYALGSDIPERCULL, ASNOFLSGNFNIEKCFOCAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  417 LEEVDDSLKLELMNYCSLLKDVDTTGTLDNYGMGNEMDIFNNLKRLI.---YHSEENINT 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49; Mismatches 104; Indels 130; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  293 EVSTKFYTDALV-LYHHINAY----EEDGHVVFDIVAYRONSLYDMF-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            373 NLVKLPISATAVKEKDGSIYCQPEILCEGIELPRVNYD-----YNGK 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 3.5%; Score 98; DB 2; Length 984; Best Local Similarity 19.1%; Pred. No. 1.1; Matches 67; Conservative 49; Mismatches 104; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        239 LONIGETGKNEKLVVYIKENILIIKWKVYGEIKOITENNKVEVHKYL
APPLICANT: COX, WILLIAM I.
IITLE OF INVENTION: RECOMBINANT VIPUS IMMUNOTHERAPY
NUMBER OF SPOURNCES: 217
                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Fatentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Frommer, William S.
PFGISTATION NUMBER: 25,506
REFERRNE//PGCKEI NUMBER: 454310-2540
TELECOMMUNICATION: INFORMATION:
                                                                                               ADDRESSEE: Curtis, Morris & Safford
STPEFT: 530 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/184,009
FILING DATE: 19-JAN-1994
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                     PC-LOSZMS-DOS
                                                                                                                                                                                                                                                                MEDIUM TYPE; Floppy disk
COMPUTER: IBM PC compatible
UPERATING SYSIEM: PC LOSZMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 425066CURTMS
INFORMATION FOR SEQ ID NO: 120:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (212) 840-3333
(212) 840-0712
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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GenCore version 5.1.6
Copyright (r) 1993 - 2003 Compugen Ltd.
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OM profein - protein search, using sw model

July 15, 2003, 09129:45 ; Scarch time St Seconds (without alignments) 1113:396 Million ceil updates/sec Run en:

US-10-053-192-1

MHILLINGH SMETPONDISARTE 526 1 METIFNENKEEHPEPIKAEV Perfect score: Sequence.

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445758 seqs, 116419773 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Listing first 45 summaries Maximum Match 100% Post-processing: Minimum Match 08

Database :

Published_Applications_AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Description	Sequence 1. Ann. 1		Sequence 5. Appli	8	Sequence A. April 1	Sequence 33, April	Sandin Orient 16. April	Sequence 10, Appl	<			, A	17	. T	Sequence 338, App		340,		
ID	US 10-053-192-1	115-10-053 192-1	118-10-053-192-5	US-09-758-269-18	US-09-758 254-8	US 09-758-269 33	US-09 758-269-16	ns-09 758-269-10	115-09 758-269-6	us-08-976-063C 22	US-09 758-269-14	US-09-758-269-4	113-09-758-269-12	US · 09 · 758 · 269 · 2	115-09-884-465A-338	11S-09-884-465A-336	US-09-884-465A-340	US-09-884-465A-342	US-Ũ9-ÄÄ4-465A-44H
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107	. co	1211	13	US 09 815 242 11451	
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106	3.8	663	σ.	US-10-121-032-61	
106	8.8	669	ħ	US-10-093-03/-01	Sequence 61, Appl
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104	 	497	ø	118-10-073-865-125	125,
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103	~	4.47	=	119-114-764-8114-276	Sequence 276, App
103	3.6	1133	Ġ	US 10:073 865 102	011
103	9.	1139	7	US-09-764-881 99	Swinence 99, Appl
103	2	5.7 I I	=	115-114-764-854-634	Sequence 644, App
504	3. F	11.59	7	US 07 264 878 204	Sequence 204, App
101.5	4.	165	्र	US-09-815-242-5366	Sequence 5366, Ap
101 5	٠,	411	_ -	115-04-815-242-12606	Sequence 12606, A
101.5	3.6	686	10	US-09-815-242-10843	Sequence 10843, A
101.5	3.6	3712	σ	US-10-108-605-103	Sequence 103, App
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100	3.5	841	10	US-09-815-242-5779	Sequence 5779, Ap
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ALIGNMENTS

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APPLICANT: FRIEDEBLY, ARD M
APPLICANT: WIFIZ, Sabraele M
APPLICANT: WIFIZ, Sabraele M
APPLICANT: WYSS, Marian
APPLICANT: WYSS, Markus
APPLICANT: WYSS, Markus
TITLE OF INVENTION FRIENCES CODING THEREFOR AND THEIR USE
FILE PREKENNE: B.B-CAROTENE IS,15'-DIOXYGENASES, NUCLEIC ACID
TITLE OF INVENTION SEQUENCES CODING THEREFOR AND THEIR USE
FILE PREKENNE: B.B-CAROTENE IS,15'-DIOXYGENASES,...
CURRENT APPLICANTON UNMERE: US/10/053,192
PRIOR APPLICANTON NUMBER: 1099:02-22
PRIOR PILLING DATE: 1999:02-22
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                       , Sequence i, Application US/lons(192) Publication No. US.no(con87336Al geneRal INFORMATION:
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Best Local Similarity 100.0
Watches FDC, Inspiration
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SOFTWARE: Patentin Ver. 2.1
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CURRENT APPLICATION NUMBER: 103/10/053,192
PRIOR APPLICATION NUMBER: 103/182.0
PRIOR APPLICATION NUMBER: 103/182.0
ILINMOTS I VDRGPTKYVI FRI PSSVPEKEKKKSGFKHI EVVGSI PSPSLLQPSYYHSFGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Publication No. US20030087336A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BACHMANN, Heinrich
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SOFTWARE: Patentin Ver. 2.1
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APPLICANT BRIDGER, AND M
APPLICANT PRIEDER, AND M
APPLICANT WIRZS, Gabriele M
APPLICANT WESS, Adrian
APPLICANT WYSS, Adrian
APPLICANT WYSS, Adrian
TITLE OF INVENTION: Hela, Hela-Camofene 15,15'-Dioxygenases, Nucleic Acid
TITLE OF INVENTION: SEQUENCES CODING THEREFOR AND THEIR USE
TITLE OF INVENTION: SEQUENCES CODING THEREFOR AND THEIR USE
CUPRENT FILING DATE: 19,47-02-22
CUPRENT FILING DATE: 19,99-02-22
NUMBER OF SEQ ID NOS: 10
SOFTWARE OF SEQ ID NOS: 10
SOFTWARE PACED AND SOFTWARE SEQ ID NOS: 10
SOFTWARE PACED AND SOFTWARE SEQ ID NOS: 10
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                                                                                                                                                                                                                                                         310 NAYEEDGHVVFDIVAYRDNSLYPMFYLKKLPKDFEVNNKLTSIPTCKRFVVPLQYDKDAE
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                                                              241 QPFKLDIVKLATAYIKGVNMASCLSFHKEDKIWFHFVDRKTRKEVSIRPTDALVLYHHI
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Publication No #S20030087336A1
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Matches 226; Conservative
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29 YOLKELLESTELEPHVNIYMEKKYKYVALFVUMSEVDEFRIAKINV21	RESULT 5 US-09-768-9.8 Sequence 8, Application US/09758269 Sequence 8, Application US/09758269 Sequence 9, Application US/09758269 Sequence 100-101-101 APPLICANT: ROBAYASHI, MASATOMO APPLICANT: GINOZAKI, KAZUO TITLE OF INVENTION: TRANSGENIC PLANTS CARYING NEOXANTHIN TITLE OF INVENTION: TRANSGENIC PLANTS GENE FILE REFERENCE: 394 - 3 CURENT FILING DATE: 2001-01-12 FRIOR APPLICATION NUMBER: JP 2001-003476 PRIOR APPLICATION NUMBER: JP 2001-00-11 FRIOR APPLICATION NUMBER: JL 2006-01-13 SEQ ID NO 8 LENDY SEQ 1D	Query Match	QY 63 ENGEVYRESKYLESIYTYNCHIFANETUVVSEPGTMAVUNCKNIFAKAETLSHTIPEFTD 122 1	2y 157 KVDYSKYVAVNLATSHEHYDS-AGNILAMGTSIVLKGFTKYVLFKIESSVPEKEKKKSGF 215 :	255 MHDPVDIIISEPIMMIDFAITETYAIFMDLPMHFRPKEMVKEKKMI 273 ;SFHFENKTWFHFVDPFTFKEUSTK-FYTDALVLYHHINAYEEDGHVVFDIVAYRDNSLY	Qy 332 DMFYL/KI,DNDFEVNNKITS:1PTCKPFVVPIQYDKDAEVGSNIJVKI,PTSATAVKFKDGST 349 1
Db 298 SPENLEHHINTYEDNGFLIVDLCCWKGFEFVYNYFTLYLANLRENWEEVKNARKAAPQPE 357 Qy 355 CKRFVVPLQYDKDAEVGSNLVKLP-TSATAVKEKDGSIYCQPELLCEGTELPRV 407 11:11:11:11:11:11:11:11:11:11:11:11:11	RESHIT 4 US-9-758-269-18 US-9-758-269-18 Sequence 18, Application US/09758269 Patent No. US2002010412041 Sequence 18, Application US/09758269 Patent No. US2002010412041 SEQUENCE INFORMATION: APPLICANT: HUGHI, SATOGHI APPLICANT: KCHAYASHI, MASATOMO TITLE OF INVENTION: CLEAVAGE ENTYME GENE FILE REFERENCE: 3914-3 CURRENT PAPLICATION NUMBER: US/09/758,269 CURRENT PAPLICATION NUMBER: US/09/758,269 CURRENT PAPLICATION NUMBER: US/09/778,269 PRIOR APPLICATION NUMBER: US/09/758,269 CURRENT PAPLICATION NUMBER: US/09/758,269 WHOBER OF SEQ 1D NOS: 33 SOFTWARE: PATENT OF SEC 2001-01-13 SEQ 1D NO 18 LENGH: 538 TYPE: PRT		56 RDETP-PVKDLPVHGFLPRECLNGFPWRGPNPKFLAVACYHWFDGGALLDSFTF 58 KDETP-PVKDLPVHGFLPRECLNGFPWRGPNPKFLAVACYHWFDGGALLDSFTF 63 KNGFVYPSKYLRSDTYNCNIEANPTVVSFFGTMAYPDFPCKNIFAKAFSYLSHTIPFFTD 109 KDGKATYVSRYVKTSRLKQEFFFGAAKFMKIGDLKGFFG	Db 157 KUDYSKYUANLATSHPHYDS-AGNILMMGTSIVDKGRTKYVIERIDSGDLGTLG 207 157 KUDYSKYVANLATSHPHYDS-AGNILMMGTSIVDKGRTKYVLERIPSSVPEKEKKKSCF 215 16	QY 216 KHLEVVCSIPSPSLLQFSYYHSFGITENYIVELEQFFKLDIVKLATAYIKGVNWASC 272 1 1 1 1 1 1 1 1 1	Db 301 YSFDPTKKARFGVLPRYAKDELMIRWPELPNCFIFHNANAWBEEDBVVL-ITCRLENPDL 359 Qy 332 DMFYLKKLDKDFPVNKLFSIFTCKRFVVPLQYDKDAEVGSNLVKLPTSATAVKEKDGSI 391 Db 360 DMVSGKVKEKLENFGNEI,YEMRPNMKTGSA 389

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DI.PVHGFI.PECI.NGEFVRVGP-----NPKFDAVAGYHWFDGDGM1HGVR1 108
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23.6%: Pred. No. 1.3e-16;
Live 79, Mismatches 213; Indels 144, Gaps
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                  449 GCNIKGIYDLGFGF-YGSEAIYVPRETA-EEDIGYLIFFVHDENTGKS-CVTVIDAKIMS 505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              360 DMVSGKVKEKLENFGNELYEM----RF-----------NMKTGSA 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           492 YCQPETICEGIELPRVNYDYNCKKYKYVYATEVQWSPVPTKIAKLNVQT------ 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 144;
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Live 79; Mismatches 213; Indels 144
                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION TRANSGENIC PLANTS CAFFYING NECKANTHIN TITLE OF INVENTION: CLEAVAGE ENZYME GENE
                                                                                                              | | : | : | : | 506 AEPVAVVELPHRVPYGFHALFVTEEQLQEQT 536
                                                                                    497 ELGRATVNV - EMHLDLHGMFIPQNDLGAET 525
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                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/758,269 CURRENT FILLIND DATE: 2001-01-12 PRIOR APPLICATION NUMBER: IP 2001-003476 PRIOR FILLNG DATE: 2001-01-11 PRIOR APPLICATION NUMBER: IP 2000-010056
                                                                                                                                                                                                                                          ; Sequence 33, Application US/09758269
; Patent No. US20020104120A1
                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: IOCHI, SATOSHI
APPLICANT: KOHAYASHI, MASATOMO
APPLICANT: SHINOZAKI, KAZUO
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NUMBER OF SEQ ID NOS: 33
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Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 3914-3
                                                                                                                                                                                                                       US-09-758-269-33
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LENGTH: 548
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449 GGNIKGIYDLGEGR-YGSEAIYVPPFTA-EEDDGYLIFFVHDENTGKS-CVTVIDAKTMS 505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 23.4%; Pred. No. 8e-14;
Matches 133; Conservative 97; Mismatches 219; Indels 120; Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.8%; Score 276; DB 10; Length 605; 23.4%; Pred. No. 8e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: TRANSGENIC PLANTS CARRYING NEOXANTHIN TITLE OF INVENTION: CLEAVAGE ENLYME GENE FILE REFERENCE: 3914-3 ENLYME GENE FILE REFERENCE: 3914-3 ENLYME GENE CURRENT AMELICATION NUMBER: US/CS/758.269 CURRENT FILING DATE: 2001-01-12 PRIOW APPLICATION NUMBER: TP 2000-010056 PRIOR FILING DATE: 2001-01-11 PRIOR AMELICATION NUMBER: 3F 2000-010056 NUMBER OF SEQ ID NOS: 33 SOFTWARE: Patentin Ver. 2.1
                                                                 497 ELGRATVNV--EMHLDLHGMPTPQNDLGAET 525
                                                                                                                                      506 AEPVAVVELPHRVPYGFHALFVTHEOLOEOT 536
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, Sequence 16, Application US/09758269
; Patent No. US:002010412041
; GENERAL INFORMATION:
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US-09-758-269-16
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APPLICANT: KOBAYASHI, MASATOMO
APPLICANT: SHINOZAKI, KAZUO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       225 VANAGVVFFNGRLLAMSEDDLPYQVKIDGQGDLETIGRFFFPDFQIFSS.....VIAHP 277
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Best Local Similarity 23.8%; Fred. No. 6.2e-13;
Matches 129, Conservative 97, Mismatches 189, Indels 128, Gaps
                                                                                                                                                                                                                                                   APPLICANT INCHI SATOSHI
APPLICANT: ROBAYASHI, MASATOMO
APPLICANT: SHINOZAKI, MASATOMO
APPLICANT: SHINOZAKI, MASATOMO
TITLE OF INVENTION. TRANSSENIC PLANTS CAFPYINS NEGXANTHIN
TITLE OF INVENTION. CLEAVAGE ENZYME GENE
FILE REPERBENCE: 3014-3
CUPRENT APPLICATION NUMBER: US/09/758,269
CUPRENT FILING DATE: 2001-01-12
PRIOF APPLICATION NUMBER: JP 2001-003476
PRIOF APPLICATION NUMBER: JP 2001-01056
PRIOF APPLICATION NUMBER: JP 2000-010056
PRIOF FILING DATE: 2001-01-11
PRIOF FILING DATE: 2001-01-13
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VOY: 2.1
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; Sequence 10, Application US/09758269
; Patent No. US20020104120A1
; GPNFRAL INFORMATION:
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                                                                                                                                           US-09-758-269-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 10
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70 RSKYLRSDTYNCNIEANRIVVS-EFGTMAYPDPCKNI-----FAKAFSYLSHT1PEFTDN 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175 PP-SACULI NAGTSTVDRGPTKYVLFKTPSSVPFKFKKKSCPKHTFVOCSTPSRLZF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           462 PHARKEHRAVULT-DEHGMETRUN 519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 CL-INIMKIGLEYY----AISEIN--FIFKIEPÖ-TLETLIPKVPYSKYVAVNLAISHPH 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 AHSTSVANASLVYENSFILLAMSELDI, PYLVQTTPNSFI, KTVGPFDFFRGOT FSTM-TAHPK-299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 YYHSFGITENYIVFIFQP--FKLDIVKLATAYIFGVNWASGLSFHKEDKTWFHFUDRKTK 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    344 MMHDFAITENFVVVFDQQVVFKL-----PFMIFG---QSPVVYGFNKVAFFGILDKYAE 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DGHVVFDIVAYPDNSLYDMFYLKKLDKDFEVN 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31 462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          403 ELPPVNYBYNGKKYKYKYVYATEVQWSPVPTKIAKLNVQTKEV-LHWGEDHCWPSEPIFVPS 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 EHPEPTKAEVQQQDPTWLQQVLLKNGPG-MHTTGDTKYNHWFLX3LALLHSFTFKNGEVYY 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            347 NKLISIPTCKPEVVPLQYPKPAEVGSNLVKLPISATAVKEKPGSIYOQPELLOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.2%; Score 260; DB 10; Length 599; 24.4%; Pred. No. 1.5e-12;
                                                                                                                                                                                                                            TITLE OF INVENTION: TRANSJENIT FLANIS CAFFYING NEGXANTHIN TITLE OF INVENTION: CLEAVAGE ENZYME GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85; Mismatches 217;
                                                                                                                                                                                                                                                                                           FILE REFERENCE: 3914-3

"UPPERNT APPLICATION NUMBER 155/14/58,269
CURRENT FILING DATE: 2001-01-12

PRIOR APPLICATION NUMBER 17 2001-003476

PRIOR PILING DATE: 2001-01-11

PRIOR PLING DATE: 2001-01-13

PRIOR PLING DATE: 2000-01-13

NUMBER OF SEQ 1D NOS: 33
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                               ; Sequence 6, Application US/09/58269; Patent No. US25020104120A1
                                                                                                                             APPLICANT: IUCHI, SATOSHI
AFFLICANT: KOBAYASHI, MASATOMO
APPLICANT: SHINOZAKI, KAZUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONCANISM: Arabidopsis thaliana US-09-758-269-6
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                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 599
JS-09-758-269-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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305 PF----PNSQNQPFAPEK------AVPRLTRWEIDLDSSSDEIKRTRLHDFFAE 448
                                                  377 LPTSATAVKEKDGSIYCQPEILCE----GIELPRVNYDYNGKKYKKYVYATEVQWSPVPT 431
                                                                                     432 KIAKLNVQTKEVLHWGEDHCWPS-----EPIFVPSPDAREEDEXVVLTCVVVSEPNKA 484
                                                                                                                                                                                   69 YRSKYLRSDIYNCNIEANRIVVSE--FGIMAYPDFG----KNIFAKAFSYLSHTIPEF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 PHYESA-GNILNMGISIVERGEFRYVLFRIFSSVFERERRRETFRHLEVVTSTPSFSILL 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232 PSYYHSFGITENYIVFIEQP--FELLETVELAIAN I POVNWASOLSEHKELE IWEHEVLEEL 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.5%; Score 239.5; DB 10; Length 604;
23.2%; Fred. No. 6.7e·11;
Live 79; Mismatches 231; Indels 111; Cups
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299 PKLDPATGELHALSYDV1KRPYLKYFYFR-----PDGTKSDD-- VEIP
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Patch No. US2022010412041
GENERAL INCRMATION:
APPLICANT: IUCHI, SATOSHT
APPLICANT: SHINOZAKI, MASALOMO
APPLICANT: SHINOZAKI, KAZUO
TITLE OF INVENTION: TRANSGENIC PLANTS CARRYING NEOXANTHIN
TITLE OF INVENTION: CLEAVAGE ENZYME GENE
FILE REFERENCE: 3914-3
                                                                                                                                                                                                                                                        485 PFLLILDAKTFKELGRATVNVEMHL--DLHGMFIP 517
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NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
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                                             GENERAL INFORMATION:
APPLICANT: Alexander Steinbuchel; Horst Priefert; Jurgen Rabenhorst
TITLE OF INVENTION: SYNTHETIC ENZYMES FOR THE PRODUCTION OF
TITLE OF INVENTION: CONIFERYL ALCOHOL, CONIFERYLALDEHYDE, FERULIC ACID, VANILLIN
TITLE OF INVENTION: ACID AND THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 HTTPEFTONCI.IN--IMKTCDDYYATSETNFIRKIDPQTLETLDKVDYSKYVAVNLATSH 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 DISVKGLDRIVANISIISHHAKVLAVKEDGLPYELDPKTLEIKGHFDYDGQVISQTHTAH 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        168 PKYDPETGDLLFFGSAAKGEATPDMAYYIVDKHGKVTH-------ETWFE-- 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 ALLHISFTFKNGEVYYRSKYLRSDTYNCNIEANRIVVSEFGTMAYPDPCKNIFAKAFSYLS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 GMASAFHFEDGHVDF1SFWVKTARFTAERLARK---SLFG--MYRNP-----YTD 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173 PHYD-SAGNII.NMGTS------IVDK-GRTKYVLFKIPSSVPEKEKKKSCFKHL 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           219 EVVCSIPSRSLLQP--SYYHSFGITENYIVFIEQPFKLDIVKLAT------AYI 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211 ------OPYGAFMHDFAITRNWSIFPIMPATNSLSRLKAKQPIYMWEPELGSYI 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              265 RGV---NWASCLSFHKEDKTW-FHFVDRKTKKEVSTKFYTDALVLYHHINAYEEDGHVVF 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              259 - GVI.APRQGSI.IRWLKAPALWVFHVVN---AWEVGTKIYIDLM------ESEILPF 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 321 DIVAYRUNSLYDMFYLKKILDKDFEVNNKLTSIPTCKRFVVPLQYDKDAEVGSNL---VK 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 FNHNKEE-----HPEPIKA-----EVQGQLPTWLQCVLLRNGBGMHTIGDTKYNHWEDGL 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 FNRNDPQLVGTLLPTFLEADLEDLEVDGELPKSINGTFFRNTPEPQ-VLPQKFHTFLDGD 62
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                                                                                                                                                                                                                                                                                                                                                                                                    E: Diskette, 3.50 inch, 2.0 MB storage HP VECTRA
                                                                                                                                                                STATE: Now ver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 196 49 655 1 (Germany)
FILING DATE: 29-NOV-1996
ATTOKNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEFEKENCE/DOCKET NUMBER: Bayer 9998-CAU TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/376,063C
FILING DATE: 21-NOV-1997
Sequence 22, Application US/08976063C
Publication No. US20020182697A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33,141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (914) 332-1700
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amino acid
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                                                                                           NUMBER OF SEQUENCES:
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OPERATING SYSTEM:
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457 IFV---PSPDAREEDEGVVLTGVVVSEPNKAPFILII.DAKTFKFI.GRATVNVEMHI.--DI. 511
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Matches 126, Conservative
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                                                                                       512 HGMFIPQNDL 521
                                                                                                                              583 HGLFVKESDI, 592
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                                                                                                                                                                                                                                                                                                                                                                                                            3914-3
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                                                                                                                                                                                                                 US-09-758-269-12
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461 SPDA----REEDEGVVLTCVVVSEPNKAPFLLILDAKTFKELGRATVNVEMHLDLHGMFI 516
                                                                                                       536 MDPAAAHPRGEDDGYVLT-FVHDERAGTSELLVVNAADIRLEATVQLPSRVPFGFHGTF1 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 IHGTLPLSLNGAYTRNGPNPQFLPRGPY-HLFDGDGMLHAIKIHNGKATLCSRYVK--TY 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187 KYNVEKQTGAPVMPNVFSGFNGVTASVARGALTAARVLTGQY-----NPVNGI----- 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 YLSHTIPEFTDNCLINIMKTGDDYYATSETNF---IPKIDPQTI:FTLDKVDYSKYVAVNL 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 GLANTSLAFFSNRL.....FALGESDLFYAVFLIESGLIEIIGKYLFLGKLAMSM 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169 ATSHPHYDS-AGNILNMGTSIVDKGRTKYVLFKIPSSVPEKEKKKSCFKHLEVVCSIPSR 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    285 -TAHPKIDPITGETFAFRYGPVPPFLT-YFRF---DSAGKKOR------DVPIF 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228 SLLQPSYYHSFGITENYIVF--IEQPFKLDIVKLATAYIRGVNWASCLSFHKEDKTWFHF 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  286 VDRKTKKEVSTK-FYTDALVLYHHINAY-EEDGHVVFDIVAYRDNSLYDMFYLKKLDKDF 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     344 EVNNKLTSIPTCKRFVVPLQYDKDAEVGSNLVKLPTSATAVKEKDGSIYCQPEILCEGIE 403
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                                                                                                                                                                                                                                                                                                                                                        APPLICANT: UCHYANGERI, MASATOMO
APPLICANT: UCHYANGERI, MASATOMO
ITLE OF INVENTION: TEANASENIO PLANTS CAEPTIN; NE XANTHIN
TITLE OF INVENTION: TEANASENIO PLANTS CAEPTIN; NE XANTHIN
TITLE OF INVENTION: CLEAVAGE ENZYME GENE
FILLE REPERENCE: 3914-3
CURRENT APPLICATION NUMBER: 05/09/75#, 244
CURRENT FILING DATE: 2001-01-12
PRIOF PLILING DATE: 2001-01-11
FRIOF APPLICATION NUMBER: 1P 2001-003-004
FRIOF PLILING DATE: 2000-01-13
NUMBER OF SEC IE NOS: 33
SOFTWARE PATENTION OF 201
                                                                                                                                                                                                                                                                                                ; Sequence 4, Application US/09758269
; Patent No. US20020104120A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97 AYPDPCKNI-----FAKAFSYLSHTIPEFTDNCL-INIMKTGDDYY-----ATSETNF-- 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       225 VEPKATGELIIGHSGTAPLLI PYAPGLPCLVPGSQGMGVANAGLVYFNNHLLAMSEDDLPY 284
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                                                                                                                  APPLICANT: IUCHI, SATOSHI
APPLICANT: KOBAYASHI, MASATOMO
APPLICANT: SHINOZAKI, KAZUO
TITLE OF INVENTION: TRANSGENIC PLANTS CAPPYING NEOXANTHIN
TITLE OF INVENTION: CLEAVAGE ENZYME GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.8%, Score 220, DB 10, 21.9%; Pred. No. 2.5e-09; tive 98, Mismatches 215,
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                                                                                                                                                                                                                                                                                                                                                                    CUPPENT APPLICATION NUMBER OBS.09/75%,269
CUPPENT FILIND DATE: 2001-01-12
PRIOR APPLICATION WHRREN 1P 2001-003476
PPICE FILING DATE: 2001-01-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: JP 2900-010056
PPIOP FILING PAIR: 2000-01-13
Sequence 12, Application US/09758269 Patent No. US20020104120A1 GENERAL INFORMATION:
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570 HGTFVDSNEL 579

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124 VEGITIPIGIDGVYIKNGAN-PMFEPTAGHHI-FDGDGMVHAVKITNGSASYACRFTKTE-- 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 -----RLVOEKPLORPVFPKATGFTHGHSCTAPLMFPYAPGTGGLTNNQNGVGVANAG 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.3%; Score 207, DB 10, Length 583, 20.2%; Prod No 2.6e-08; Live 91; Mismatches 206; Indels 142; Gaps
                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: TRANSGENIC PLANTS CARRYING NEOXANTHIN
TITLE OF INVENTION: CLEAVAGE ENZYME GENE
FILE REFERENCE: 3914-3
CURRENT APPLICATION NUMBER: US/09/758.269
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: JP 2001-003476
PRIOR FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: JP 2000-010056
PRIOR FILING DATE: 2001-01-13
NUMBER OF SEQ ID NOS: 33
SOUTHWARE: PATENTIN VET: 2.1
                                                   574 LQIVNAQNLKLEASIKLPSRVPYGFHGTFIHSKDL 608
487 LLILDAKTFKFLGRATVNVEMHLDLHGMF1PQNDL 521
                                                                                                                                                                                         ; Sequence 2, Application US/09758269; Patent No. US20020104120Al; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                   APPLICANT: IUCHI, SATOSHI
APPLICANT: KOHAYASHI, MASATOMO
APPLICANT: SHINOZAKI, KAZUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Arabidopsis thaliana US-09-758-269-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches Ili; Conservative
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                                                                                                                                                            US-09-758-269-2
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Best Local Similarity 21.4%, Fred. No. 3.8;
Matches 135; Conservative 76; Mismatches 245; Indels 174; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Streptococcus Antigens FILE REFERENCE: 055190-0044 CURRENT APPLICATION NUMBER: US/09/884,465A CHRPENT FILIN3 DATE: $\tilde{2}\tilde{0}$.
                                                         Sequence 338, Application US/09884465A Publication No. US20030077293A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPICE APPLICATION NUMBER. 60,212,683
PRICE FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SEQ ID NO 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Unknown Organism US-09-884-465A-338
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Martin, Denis
APPLICANT: Charland, Nathalic
APPLICANI: Ouellet, Catherine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                      APPLICANT: Shire Biochem, Inc. APPLICANT. Hamel, Jusee
                                                                                                                                                                                                                                                                                                                                    Brodeur, Bernard
                                                                                                                                                                                                                                                                                      Hamel, Jusee
                                                                                                                                                                  GENERAL INFORMATION:
US-09-884-465A-338
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Search completed: July 15, 2003, 09:39:20 Job time: 57 secs



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OM protein - protein search, using sw model

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671580 seqs, 205047115 residues Searched:

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671580 Total number of hits satisfying chosen parameters:

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Post-processing: Listing first 45 summaries

SPTREMBL_21:* Database :

sp_human:*
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sp_bacteria:*
sp_fungi:* sp_organelle:*sp_phage:* sp_plant.* sp_rodent.* sp_virus.*

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sp_rvirus.* sp_bacteriap:*

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SUMMARIES

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ALIGNMENTS

	10 091993 II	PRELIMINARY:	 2.	525 AA.	
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	01-0CT-2000	(Tremetrel, 15,	(reated)		
	01-001-2000	(Irembhrel 15,	Last sedu	mence update;	
	01-DEC-2001	(Tremelrol, 19,	Last anno	01-DEC-2001 (TrEMPLrel. 19, Last annotation update).	
DE	Seta caretene	Beta carotene 15,15' - dlaxyvenuse (EC 1.13,11,21),	Hinse (ET	1.13.11.21).	
	BCDO.				- ,
_	Gallus gallus (Chicken).	s (Chicken).			
	Pukaryota, Me	stassa; Chordat	a; Craniat	Eukaryota, Metasoa; Chordata, Crasiata, Vertebrata, Buteleostomi;	eleostomi;
7 50	Archesauria;	Aves; Necquath	ae; Gallif	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;	Phasianinae:
	Gallus.				
	NCBI_TaxID=9031;	331;			
N.A.	[1]				
	SECUENCE FROM N.A.	A N.A.			
	SIFAIN=LSL LC	SIFAIN=LSL LOHMANN; IISSUE=DUODENUM;	DUCCENUM;		
	MEDILINE-2026	MEDIINE-20261261; PubMed-10799297;	1263562		
	Wyss A., Wirt	zz C.M., Wogger	W.D., Bru	Wyss A., Wirtz C.M., Woggon W.D., Brugger R., Wyss M., Friedlein A.,	riedlein A.,
	Bachmann H.,	Bachmann H., Hunziker W.;			
	"Cloning and	expression of	heta, heta	and expression of beta, beta carotene-15,15'-dioxygenase.	oxygenase.";
KL .	Bicchem Bior	Blophys Res Commun 271 : 14- 116 (2000).	un. 271.44	14-446(2000).	
RN	[2]				
	SEQUENCE FROM N.A.	4 N.A.			
RC S	STRAIN=LSL L(STRAIN-LSL LOHMANN; IISSUE-DUODENUM;	DITODENUM;		
	MEDLINE=21134	MEDLINE=21134366; PubMed-11237856;	237856;		
PA v	Wyss A , Wirt	.z G M , Woggor	W P , Br.	Wyss A , Wirtz G M , Wodgon W D , Brugger P., Wyss M., Friedlein A.,	riedlein A.,
	Riss G., Bacl	Riss G., Bachmann H., Hunziker W.;	ker W.;		
	"Expression	safferin and los	411174116	"Expression pattern and localization of beta beta-carotone 15,15'-	410 15,15'-
P.T.	dioxygenase	dioxygenase in different tissues.";	senes.		
	Richten J	Bisabem J 354 521-529(2001).	1).		
	EMBL, AJ27136	EMBL, AJ271386, CAR99827.1;			
DR 1	InterPro; IP	InterPro; IPPS04294; PPE65.			
퍞	Piam; PP∪∢05°	Pfam; PP∪ (055; PPP65; 1.			
F.W.	Cleary probable.	Oxi loreductase			
ş	SEQUENCE 8	SEQUENCE SEC AND KITHER MW.		HICHEAAP75FE345B CRC64;	

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                                                                                                                                                                                                                                                                                                                    DALVLYHHINAYEEDGHVVFDIVAYRDNSLYDMFYLKKI,DKDFFVNNKI,TSIPTCKRFVV 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 TEKNGEVYYRSKYLRSDTYNGNIEANRIVVSEEGIMAYPDPCKNIFAKAFSYLSHTIPEF 120
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                                                                                                                                                                                                                                                                                                    241 TENYIVELEQPEKLDIVKLATAYIRGVNWASCLSFHKEDKTWFHFVDRKTKKEVSTKFYT 300
                                                                                                                                                                                                                                                                                                                                                                                                  301 DALVLYHHINAYEEDGHVVFDIVAYRDNSLYDMFYLKKLDKDFEVNNKLTSIPTCKPFVV 260
                                                                                                                                                                                                                                                                                                                                                                                                                                    44. PLQYDKDAEVGSNI VKLPTSATAVFEKDOSTYOQPELLCEGTELPPVNYDYNGKKYKYYY 420
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   Gaps
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"Cloning and characterization of a human beta, beta-rarotene 15,157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota: Metarea: Cherdata: Craniata; Vertebrata; Puteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-MAR-2001 (TTEMBLEEL 16, Last sequence update)
01-JUN-2002 (TTEMBLEEL 11, Last anneration update)
Beta, beta-carotene 15,15'-dioxyqenase (EC 1.13.11.21).
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   0; Mismatches
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Ptam; PF03055; RPE65; 1.
Matches 526; Conservative
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Isogai T., Ota I., Hayashi K., Sugiyama T., Ctsuki T., Sutuki Y., Nishikawa T., Nadai K., Sugano S., Shiratori A., Sudo H., Waqatsuma M., Hosolii T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Chiba Y., Ishida S., Murakawa K., One Y., Takiquehi S., Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saite K., Wamanoto J., Makamatsu A., Nakamura Y., Naqahari K., Masuho Y., Ninomiya K., Iwayanaqi T.; Nakamura Y., Naqahari K., Masuho Y., Ninomiya K., Iwayanaqi T.; Nakamura Y., Naqahari K., Masuho Y., Saitha K., Saitha Y., Saitha K., Saitha K., Masuho Y., Nagahari K., Nagahari K
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J. Biol. Chem. 0:0-0(2001).
EMBL. AIT/8064, CAROCCELLO:
EMBL. AF271298; AAG33982.1; -.
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STRAIN-CS7BL: TISSUE-KIDNEY;
Wyss A., Wirtz G.M., Woggon W.D., Brugger R., Myss M., Friedlein A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL; Redmend T , Pu S , Wiggert B., Gantl E.,
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"Expression pattern and localization of beta,beta-carotene 15,15'-
dloxygenase in different tissues.";
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Mammalia; Eutheria; Rodentia; Sciuroqnathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 547;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (DEC-2000) to the EMBL/SenBank/DPBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR094294, RPE65.
Pfam; PF03055; RPE65; 1.
SPQUENTE - 547 AA; h2574 MW; 444AlmHullishbABF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ni-uxi-2000 (TrEMBLre) 15, created)
01-MAR-2001 (TiEMBLre). 16, Last sequence update)
01-JUN 2002 (TrEMBLrel. 21, Last annotation update)
Beta beta carotene 15,15' dioxygenase (EC 1.14.11.21)
RCDOLOR RCDO OR BCDO.
                                                                                                                                                                         (TrEMBLrel. 15, Last sequence update) (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
                                                                     547 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          566 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 25;
; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 NIEANRIVVSEFGIMAYPDPCKNIF 106
                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Last annot
CDNA FLJ10730 fis, clone NT2RP3001307
                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPT;
                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR004294; RPE65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25; Conservative
                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF03055; RPE65; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:1926923; Bcdol
                                                                                                                                                                                                                                                                            Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cunningham F.X.;
                                                                                                                                                                     01-OCT-2000
                                                                  Q9NVH5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       697786;
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RESULT 3
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                                    Q9NVH5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93136
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SEÇUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09NKW9;
                                                                                                                                                                                                                                                                                                                                                                                                          B-DIOX
                                                                                                                                                                                                                                                                         090WH4
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                                                                                                                                                                                                                               RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best
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                                                                                                                                                                                                                                                      090WH4
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"Regulation of beta-carotene 15,15' dioxygenase in exidative stress",
Submitted (JUN 201) to the EMBL/Schrank, PDBJ dat Bases
EMBL: AB662912; BAB66804.1; -.
InterPro: IPP004294; RPE65.
Pfam: PP03055; RPE65; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia, Eutherla, Rodentia; Sciurognathi, Maridae, Murinae, Katius.
NCRI_TaxID=10116;
                                                                                                                   GAPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yan W , Jang G -F , Hansologi F , Esumi N , Chang ! , Korrigan M , Campochiato P , Palozewski K, Zack D J , Eloning and characterization of a human belo, but a calcing dioxygenase that is highly expressed in the retinal pigment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                   3
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                                                               4.8%, Socie 25, LB 11, Lougth 506, 100 0%, prod No. 2.1e-18;
Live 0: Mismatches 0; Indets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.8%; Score 25; DB 11; Length 566, 100.0%; Pred. No. 2 1e-18;
                                                                                                            d; Indets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                epithelium.";
Submitted (ANG-2006) to the EMBL/GenBank/DDBJ databases
EMBL; AF294899; AATISARII;
MGD; MGLI926923; BGG01.
InterPro; IPRON4294; RPEK5
Ffam; FF03055; RFEEE; 1.
                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Beta, beta-carotene 15,15'-dioxygenase (EC 1.13.11.21).
Dioxygenase, Oxidoreductase.
SEQUENCE 566 AA; 61864 MW; 184367815247ARD: PPF44,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        566 AA; 63852 MW, LC4D+791RC4567UD CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         566 AA; 63637 MW; AIFF8A47BA6CE6E5 CPC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19) Last sequence update) (I-MAK-2002 (TrEMBLrel. 20, Last annotation update) Beta-carotene 15,15,~djoxygenase.
Pattus norvegirus (Pai)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Pred. in
                                                                                                                                                          82 NIEANRIVVSEFGTMAYPDPCKNIF 106
                                                                                                                                                                                82 NIEANRIVVSEFGTMAYPDPCKNIF 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82 NIEANRIVVSEFGTMAYPDPCKNIF 106
                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMPLrel 16, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                   PPT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL; TISSUE=KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dioxygenase; Oxidoreductase.
                                                                                    Best Local Similarity 100 (
Matches 25, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                 PPELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=INTESTINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                BCD01 OF RCPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dioxygenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                 Querry Mateh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                        09ERN9;
                                                                                                                                                                                                                                                                                                                 POPPNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    091XT5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
                                                                                                                                                                                                                                                                                            Q9ERN9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDINE=11216714; PubMod=11278918; Kinferor M.D., Kinferor M.D., Hassel S., Lampert T.M., Vegt K., Inderor M.D., Breithaupt D.E., von Lintig J., Breithaupt D.E., von Lintig J., Breithaupt D.E., von Cand Characterization of a Munmalian engine catalyzing the asymmetric exidative cleavage of provitamin A."; J. Biol. Chem. 276:14110-14116(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Tracheata; Hexapoda, Insecta;
Pterygota, Neoptela; Endopterygota, Diptera, Brachycera, Muscomorpha;
Ephydroidea; Drosophilade; Drosophila.
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukarycta, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopteryqii, Neopteryqii, Teleostoi, Ustariophysi, Cypriniformes, Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ú; Caps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , Match 2.5%; Score 13; DB i3; Length 516; Local Similarity 100.0%; Pred. No. 4.2e-05; les 13, Conservative 0; Mismatches 0; Indels
  Length 566;
                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              516 AA; 58584 MW; DEDA47707E55C93F CRC64;
                                                                                                                                                                                                                                                                                                                               0.0 DEC 2001 (TrEMBLED). 19, Created)
01-DEC-2001 (TrEMBLED). 19, Last sequence update)
01-MAP-2002 (TrEMBLED). 20, Last annotation update)
Putative b,b-carotene-15,15'-dioxygenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01.0CT-2000 (TrEMBLrel. 15, Created)
01.0CT 2000 (TrEMBLrel. 15, Last sequence update)
01.DEC-2001 (TrEMBLrel. 19, Last annotation update)
4.8%, Scott 35, PR 11; 1
Best Local Similarity 100.0%; Pred. No. 2.1e-18;
Matches 25, Conservative of Mismatches of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brachydanio rerio (Zebrafish) (Zebra danio).
                                                                                                                                                                                                                                                                                         516 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       620 AA
                                                                                                         82 NIEANKIVVSEFGIMAYPOPCKNIF 106
                                                                                                                                                          82 NIEANRIVVSEPGTMAYPDPCKNIF 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPT;
                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL: AJZSU3SU; CAC3/566.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR004294: RPE65.
Pfam, PF03055; RPE65, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 GTMAYPDFCKNIF 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94 GTMAYPDPCKNIF 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPRÉS OR DRPRÉS OR CG9347.
                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINAPY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dioxygenase.
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METAIN-HERELLEY,

RAMENIA-HERELLEY,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adamstides F.G., Selerer S.E., Highway, Hoskins R., Aralle P. F.,

RA Groote R.A., Lewis S.E., Etchards S., Ashburner M., Henderson S.N.,

RA Stricus G.G., Wortman J. R., Yandell M. D., Zhang O., Chen T.X.,

RA Hardon R.C., Rogers Y.-H.C., Blazely R.G., Champe M., Pfefffer B.D.,

RA Harli J.F., Agrayania A., An H.-J., Andrews-Flankoch C., Baldwin D.,

RA Ballew R.M., Remus P. V., Bernan B. P., Hhandari U., Holshakov S.,

RA Bersou K.Y., Benus P. V., Bernan B. P., Hhandari U., Holshakov S.,

RA Bersou K.Y., Benus P.V., Bernan B. P., Hhandari U., Holshakov S.,

RA Bersou K.Y., Benus P.V., Bernan B. P., Handari U., Holshakov S.,

RA Berson K., Doup L.E., Downes M., Duan-Rocha S., Dunkov B.C., Dunn P.,

RA Chorfy J.M., Cavaleys S., Dablyor C., Reperson D.,

RA Harris M.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann C.,

RA Harris M.L., Harvey D., Howland T.J., Meri M.-H., Ibegwam C.,

RA Jalai M., Kalush F., Karpen G.H., Ne. S., Kalp R., Lin X.,

RA Jalai M., Kalush F., Karpen G.H., Ne. S., Kenle M. H., Lin X.,

RA Jalai M., Kalush F., Karpen G.H., Ne. S., Kenle M. H., Lidar Y., Lin X.,

RA Jalai M., Kalush F., Karpen G.H., Ne. S., Norkis J., Moshrefi A.,

RA Mount S.M., May M., Murphy R., Murphy R., Morpherson D.,

RA Mount S.M., May M., Murphy R., Murphy R., Markon M.,

Spier E., Siden-Klamos I., Simpson M., Strong C., Shen H.,

Spier E., Staden-Klamos I., Simpson M., Strong C., Zhao Q., Zhao Q., Zhao Q., Zhao G., Zhao R.,

RA Spier E., Shauling A. P., Zhan M., Zhang A.H., Wang A. A.,

Mulliams S. M., Wassarman D.A., Weinston B.C.,

RA Spier E., Salen-Klamos I., Shan M., Zhang S., Zhao Q., Zhao Q., Zhao G., Zhao R.,

RA Spier E., Salen-Klamos I., Shan M., Wenes C.,

RA Spier E., Salen-Klamos C., Chan W., Wenes M., Shang R.,

RA Spier E., Salen-Klamos C., S
                                                                  c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    iterydota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Grosophilidae, Drosophila,
NCBI_TaxID~7227;
                                                                  Gars
                                                                c`
                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryöta, Metazoa, Arthropoda, Trachosta, Hexapoda; Insenta;
                2.1%; Score 11; DB 5; Length 620; 100 0%; Pred No 0 0083; utive 0; Mismatches 0, Indels
                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DET-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                        CG9347 protein (15,15' beta carotene dioxygenase).
RPE65 OR BETA-DIOX OR CG9347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     von Lintig J., Voqt K.;
#Filling the gap in vitamin A research.";
J. Biol. Chem. 275:11915 11926(2000)
EMRL; AE0017701; AAFS4978 1;
                                                                                                                                                                                                                                                           PKT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20229792; PubMcd-19766819;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 287:2185-2195(2000)
Guery Match
Hest Local Similarity 100 m
These 11, Conservative
                                                                                                          453 PSEPIFVPSPD 463
                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BERKELEY;
                                                                                                                                                                                                                                                             O9VFS2
                                                                                                                                                                                                                    RESULT 9
                                                                                                                                                                                                                                         O9VFS2
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Riefer C., Hessel S., Lampert J.M., Vogt K., Lederer M.O., Breithaupt D.E., Von Lintig J., "Identification and Janlackerization of a Manmalian encyme estalyzing the asymmetric oxidative cleavage of provitamin A.";
                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chórdata, Craniata, Vertebrata, Enteleostomi,
Archosaulia, Aves, Necquathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Investigation of an endoplasmic reticulum related protein in the vertebrate retinal pigment epithelium.";
Thesis (1998), Institute of Medical Science, The University of Tokyo.
EMBL; 8017594; BAA75661.
                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brachydanio refi (febralish) (febra lunin).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euroleostomi:
Arlinopterygli: Nerpterygii: Teleostei, Ostariophysi, Cyprinitormes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.9%; Score 10; DB 13; Length 533;
100.0%; Pred. No. 0 092;
                                                                                                         2.18; Score 11; DB 5; Length 620; 100 08; Prod No 0 0083; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; indels
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SEUJENCE 533 AA; 60930 MW; 67ECA3B5993084AU CRC64;
                                                                             9187228R102C31C3 CRC64;
                                                                                                                                                                                                                                                                                                                                 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLE) 19, Last sequence update)
01-MAR-2002 (TrEMBLE), 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Pred. no.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     549 AA.
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                                                                                                                                                                                                                                                                                                                   01-MAY-1999 (TrFMPLr-1 10, Created)
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                                                                                                                                                                                                                                                                                    PPT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE:21216714, Pubmed-11278918;
EMBL; AJ276682; CAB93141.1; -: FIYRASS-; FRANGO38171; RPESS. InterPro; IPP004294; RPESS. Pfam, PF030575; RPESS, 1
                                                                               520 AA; F4441 MW;
                                                                                                                           Best Local Similarity 100 Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                         453 PSEPIFVPSPD 463
                                                                                                                                                                                                       550 PSEPIFVPSPD 560
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                                                                                                                                                                                                                                                                                    PPELIMINAPY;
                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hirosawa K., Sagara H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97 AYPDPCKNIF 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 AYPEFSKNIF 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                              RPE65 protein.
RPE65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-LIVER;
                                                                 Dioxygenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-EYE;
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                                                                                SENTENCES.
                                                                                                              Ouery Match
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                                                                                                                                                                                                                                                                                                     Q9YGX2;
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SEQUENCE FROM N.A.

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The AcrA/AcrB/TolC efflux pump participates in multidrug resistance
in Enterobacter aerogenes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria, Firmicutes, Actinobacteria, Actinobacteridae,
Actinomycetales: Streptomycineae, Streptomycetaceae, Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterobartei aerugenes (Aerobarter aerogenes).
Bacteria; Protecbacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ·;
                                                                                                                                                                                                                                                                                                                        1.9%, Score 10; DB 13; Length 549;
tuv.u%; Pred. No. 0.095;
tve 0; Mismatches 0; Indels
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Thomson N.R., Parkhill J., Rarrell R.G., Pajandream M.A.,
Thomson N.R., Parkhill J., Rarrell R.G., Pajandream M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 8; DB 2; Length 169;
Pred. No. 5.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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EMBL: AJ306389; CAC35722.1; -.
NON_TER 169 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oliver K , Harris D .;
Submitted (NOV-1999) to the EMRL/GeoBank/DDRT databases
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                                                                                                                                                                                                                                             549 AA; 62326 MW; 684FCAD1BF87DBB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 169 AA; 19014 MW; 33EBC250079FD0E5 CRC64;
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01-MAY-2000 (TrEMBLrel 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
putative binding protein dependent transport protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 AA.
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                                                                                                                                                                                                                                                                                                                                                                                     luu.u*; Pred. No. U.U
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Matches 8; Conservative 0, Mismatches
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J Ricl. Chem. 275:14110-14116(2001).
EMBL: AJ290391; CACG7567.1;
InterPro: IPP0A424; PPE55.
Pfam; PF03055; RPE65; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 NRIVVSEFGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 NRIVVSFFGT 95
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                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
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                                                                                                                                                                                               Dioxygenase.
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                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                            Query Match
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"A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                      PERTINA 3(2) / M145;
Bentley S.D., Chater K.F., Cerdeno-larraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quall M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'Complete genome sequence of the model actinomycete Streptomyces
                          STRAIN=A3(2);
MEDILIGE-97000351; PubMed=8843436;
Redenbach M., Kleser H.M., Denapaite D., Eichner A., Cullum J.,
Kinashi H., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.5%; Score 8; DB 16; Length 287; 00 0%; Prod No. 8.6; vc. 0; Mismatches 0, (ndels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31533 MW; 77AB4EDECOFFA6CF CRC64;
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01-JUN-2001 (TFFMBLrel. 17, Last Sequence update)
01-JUN-2002 (TFFMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  293 AA.
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InterPro: IPR000515; BPD_transp.
Ffam, PF00528; BPD_transp: 1.
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Nature 417:141-147(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         287 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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REPRESENTATION OF THE STANDS O
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Eukaryota: Metazoa; Arthropoda: Tracheata; Hexapoda; Insecta;
Pteryota: Neoptera: Endopteryyota; Diptera; Brachyeera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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100.0%; Prod No 9 9;
tive 0; Mismatches 0; Indels
                                                                             NON_TER 293 293 SEQUENCE 293 AA; 33281 MW; F4B867CDEF4A3E7D CRC64;
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01-DEC-2001 (FFEMBLEC), 19, Last sequence update)
01-MAR-2002 (FFEMBLEC), 20, Last annotation update)
                                                                                                                                                                                                                                                                                                 PKT; 333 AA.
Nature 409:685-690(2001).
EMBL; AK020906; BAB32248.1; -.
MCD; MCI:1925068; Aq30079106Rik.
InterPro; IPRO04294; RPE65.
Pram; PF03055; RPE65; 1.
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Hest Local Similarity 100.5
For 8; Conservative
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Q95RP9
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Search completed: July 15, 2003, 09:42:43

Job time : 86 sers

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GenCore version 5 1 6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

July 15, 2003, 21-28-47 , Search time 787: Seconds (without alignments) 11502.837 Million cell updares/sec Pun on.

US-10-053-192-2 3111 Title: Perfect score·

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OLIGO_NUC Gapop 60.0 , Gapext 60 Ω Scoring table:

2054640 seqs, 14551402878 residues Searched:

Total number of hits satisfying chosen parameters: Word size .

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Minimum DB seq length: \hat{n} Maximum DB seq length: $2(n/n)\mu_1\mu_1\mu_1\mu_1$

Post-processing: Listing first 45 summaries

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1: gf. ba *
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gh_ro:* gh_sts:* gb_sy:*

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is the number of results predicted by chance to have a Ç. Pred

score greater than or equal to the score of the result being printed, and is derived by analysis of the total search distribution.

SUMMARIES

x	on	AJZ71386 Gallus qa	Sequence			ARIO/3/9 Sequence		Solanum				Sequenc		AX175501 Sequence			Arter Pattus no	AX28490/ Sequence	AX361301 Sequence	Ak051505 Sequence	AF97754F Sequence	AF 77190 Sequence	AX443514 Sequence AXeRub03 Sequence	AR167247 Sequence	AR172477 Sequence	AR167246 Sequence	AXZE1854 Sequence	AXI98908 Sequence			U36623 Human tyros	AXI48656 Sequence						55841 S	~ c	Traf	75		
SUMMARIES		GGA271386	AXOSSBLL	R[am;27]5	AR112509	AR13/3/9 AP201985	RNEGP314H		AP079853	AF015523	AP101963	APP23984	O. F. HUSH	AX175501	AX175602	HSA245567	Ar'114 / R. F.	AX28490/	AX361301	AFUS 1505	AP072:45	APU 24190	AXAGULTA	AR167247	AE172437	AR167246	AXZELED4	AXIGRADE	AX198918	AX198999	HSU36623	AX:4X54	AXIGNA41	AX198571	374	AX198825	AX365606	AX455841	1536	1221	ALIGNMENTS		
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bdb0 gene; beta-carotene 15,15'-dioxygenase. gene). AJ271386 AJ271386.1 GI:7799040 chicken. KEYWÜKDS SOURCE ORGANISM ACCESSION VERSION

REFERENCE SHUHLIIV

Callus gallus Eukaryota, Metasoa, Cherdata; Cramiata, Vertebrata; Euteleostomi; Archosauria, Aves, Neognathae; Galliformes, Phasianidae; Phasianinae; Gallus, 1 (bases 1 to 3111) Wyss,A. Wirte, G., Woggru, W., Pruggrr, P., Wyss,M., Friedlein,A.,

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Submitted (18-JAN-2000) Wyss A., Vitamins and Fine Chemical Division, VFHC, F. Hoffmann-La Roche Ltd., Building 93/814, CH-4070 Basel, SWITZERLAND
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/translation="METIFNRNKEEHPEPIKAEVOGOLPTWLOGVLLRNSPGMHTIGD
TKYNHWFDGLALLHSFTFKNGEVYPSKYLPSDTYNCNTFANPIVVSEFGTMAYPDPG
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CWPSEPTFVPSPDAREEDEGVVLJCVVVSEPNKAPFLLTLDAKTFKELGRATVNVEMH
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Rinchem Rinchys Rvs Commun. 271 (2), 334-336 (2000)
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                                                                                             2 (bases 1 to 3111)
Wyss,A., Wirtz,G.M., Woggon,W.D., Brugger,P., Wyss.M.,
Friedlen,A., Riss,G., Bachmann,H. and Hunziker,W.
Expression pattern and localization of beta,beta-carotene
15,15'-dloxygenase in different tissues
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/db_xref="GI:7799041"
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/clone="dioxy25"
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HITTHITHITHITHITHITHITHITHITHITHITHITHIT	1381 AAGTATGTCTATGCAACASAAAHCCAATASASCCAGITACCTAASAAGATGGAAAACIG 1440 HILIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	1441 AATGICCAAACAAAGAAGAACACTGGGGGAAAGACCACTGCTGGCCCCCCGGGAGCCC 1500 	1501 ATCITTGTFCCGAACCCCARGCAAGAGAAGAGATGAAGGTGFCGFTGFTGGCFGFGFT 1560 	1561 GTGGTGTC1GAGCCAAATAAAGCACCCTTCCTACTCGTCTTGGATGCTAAAACATTCAAA 1620 	GAATTGGGCCGAGCCACAGTTAACGTAGAAATGCATCTGGACCTGCATGGGATGTTTATA	1681 CCACAGAAIGATTIGGGGGGCTGAGAGGGGAATAAAAGGCTATTGATGCGACTACACAAACT 1740 	1741 GAGACAACTITGTACIGAACAIGAGIIAAYALCOCTITTAGGATGAAGAACAACATAT 1800 	1801 AACSACACAAAFSACIALGIALAATCICTIAAALAATAIAATACETETAAGGCAC 1850 	1861 AGGGATGAGTTTTACTACAGGTAAACGATATGCACAGGCATATAGATATTCCAAAAGA 1920 	1921 AGAAGAACGATGACRAFTTAGAAGTGCTAATGTTGTACATAACGGGGGGGGGGGAACA 1980 		2041 TATTTATGGTGATGCATGCATGAGTGACATAGGTCTGCAGGTATCTTTAGA 2100 	2101 GAPOGETEVARGATEGVAGCHSPSATGAVETEGTOVAGCGASAAAGCGGGFETETA 2150 HHIHHHHHHHHHHHH 2101 GALGGITTGAAGATEGGAGCFISIGATGGGAGTETTCTCCGAGCGAGAAACCTGATFFFA 2150	2161 AACCATCTOCTACTOSTAAFICATACCAATGSATTTICHOSBORIOSAGHTGACACUSTA 2329 	2221 ACCAAACITAACTATTGASSISCIACAACITCTAATTTGAACGGAACAAACA 2280 	2281 AGANARONYACH DANTTANTANDONASORIGIARTTINDONTOTTANGAROKA 240 HILLIHIHHHHHHH 2281 AGANAGAGACHSCTINGCIANIAACCCATGEIGITTITICITTITATGAIGACA 2340	2341 AAACCAAGTACATAIGGITTAIAIGIAGCAFICAATTATACTICAGIGCTATTCCATCCTA 2400 	2401 ATGTATAAGCAATTTGTATTTAAATCAGTTTTCCTTGAGAATATCTGACATATT 2460
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qq	1561	SATGTCTGAGCCAAATAAAGGACCTTCCTACTCATCTTGGATGCTAAAACATTCAAA
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Οy	1921	AGAAGAAGGATCAGTGTTTTAGAAGTGTGTAATGTTGTACATAAGGGGGGGG
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Qy	1981	GGAGAGAGAAAGGTAAGGGGAATATTTAATAGAATATAGATTTCTGAGCAAATGAAGTGCAA. 2040
ad	1981	GGAGAGAAAGGTAACGGGAATATTAATAGAATATAGATTTCTGAGGAAATGAATG
Oy	2041	TATTAIGGIGIGATGCATGGCATGACATAGGTCACATAGGTCACATGTATATATA
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Οy		GATGCAAGTTTTCTCCAGAAAAACTTCTTA
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Alitalo, K. and Jouk
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Alitalo,K. and Joukov,V.
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Patent: US 6245740 A 25 12 HR-250);
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Zoller, M.
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Mammalia: Eutheria: Rodentia; Sciurognathi; Muridae; Murinae;
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PAT 31-AUG-2000
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Proc. Natl. Acad Sci. U.S.A. 94 (20), 11079-11084 (1997)
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                                                                                                                                                                                                                                                                                       1 (bases 1 to 1982)
Schroeder, J. 1., Antosiewicz, D.M., Schachtman, D. P. and Clemens, S.
Nucleic acids encoding metal uptake transporters and their uses
Patent: US 5965792-A 1 12-oct-1999;
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Schachiman.D P , Kumar.P , Schroeder,J.I. and Marsh,E.L.
Direct submission
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/product="low-affinity cation transporter"
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VPLDDAQNITDDTRIRAAIPTTKHLIANGAKVILSSHLGRPKGVTPKYSLAPLVPPLS
ELLGIQVVKADDCIGPEVEKLVDSLPEGGVLLLENVRFYKEEEKNEPEFAKKLASLAD
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KVSSKIGVIESLLEKCDI.LLGGGM.FTPYRAQGLSVGSSLVPEDKLELATSI.LEKAK
KVSSILLESDVV.LADKPADANSKI.VPASAI.PDGWMGI.DIGPDSITFTNDALITTKT
VIWNCPMGYPEFDKR.KTGTERAI.KKI.ADLSSKGYTTI.IGGDSVAAVEKVGVASVWSH
ISTGGGASI.ELLEGKVI.PGVTALDPADAPAV."
                                                                                                                                                                                   /translation="MAPPKALAFGIII-AVVTATIAAAQKDWWYKIJSPWFNFN
                                                                                                                                                                                                      ECQCTSYGTQNTV1CSKLASKCI,VMKAEMTHSKSGRRWKPEGA1QNNDGLYDPECDEQ
GLEKAKQCNGTATCWCVNTAGVPRTDKDTETTTSEFVPTYW111ELKHKEPAQPYNFF
                                                                                                                                                                                                                                              SLHTALQDTFASRYMLNPKFIKSIMYENNVITIDLMQNSSQKTQDDVDIADVAYYFEK
DVKGESLFHSSKSMDLRVNGELLDLDPGQTLIYYVDEKAPEFSMQGLTAGIIAVIVVV
VLAVIAGIVVLVISTRKRSAKYEKABIKEMGEIHRELNA"
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Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots;
Asteridae: euasterids 1: Solanalus; Solanareae; Solanum
1 (bases 1 to 1730)
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mKNA encoding chloroplast protein, complete cds.
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/protein_id-"AAC26785.1"
/db_xref-"GI:3328122"
                                                                                                                                                                                                                                                                                                                                                                    Length 1524;
                     /tissue_type="colon cardinoma"
/elone_lib="oligo-dt-primed cDNA in pcDNA3"
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                                                                                                    /product="EGP-314 protein homoloque"
/protein_id="cAAu4496 1"
/db_xref="G1:2764585"
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Pred. No. 7.3e-08;
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Hest tacal Similarity 100.0%, Fred. No. 7.2e-08,
Matches 36, Conservative 6, Mismatches 9;
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/cell_line="regressor"
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/tissue_type="leaf"
209. .1657
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100.0%;
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1 CGGATCCACTAGIAAGGGGCGGCGCAGTGTGTGGGGGAAF 36

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KITSCTTNSAEGGLVOULFSAEKSKVSGAPTAVYTAMETMIGOUSUSAAALIEGABS
KVANRRLRQLJVWAIRLANAFULGSLAGAAFAASFAVIPGOIFAAFGPLAITAVIGLI
ALHCTVRFGEADPRNGENQKARLKVMEUMASKVTAATIJGAIMSVLAGSVGEEHHEKKG
ALDAFWVLTSTFVSSFGFMLLAAAPSSARVYLAPVSKVLIMSSVALFGATAVSVYSA
BISRAVSQ"
                                                            LKFIFSLLLAIATFFSGTALTLLSMNIVGLPESLVSAGQLVASKCLFLICTALSAMTL
VSLLALLPSMLYLCLGLVVWTVVVLPAIVVHCYMKH1FBGGDEAAALEBHKEELEAAS
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/translation="MTAPPPPPPPPTAKWSVAGHGSLMTAPPPPPPPPPARWSVAGDGS
            LMTTPPPPPPTAPWSVAGDGSLMKAPPPPPPPPPPTAPWSVAGGGSLM9APPTPLSPE
                            RLALPYQFGEPPATTDELSMRPTSSPPPTSAEETQGAFFSSVSPAPVTTGMATSFGPS
                                              TLIEAEEGRATERKEIVVKLLKARAKPNI.ELGGIAAIFGFAVI.FGWSGFPFFMKPPGN
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Christgau, S., Kofod, L.Venke., Andersen, L.Nonboe., Kauppinen, S.,
Heldt-Hansen, H.Peter and Dalboege, H
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Lowenthall, William., York, J.Joy., O'Neil, T.Ellen., Phodes, S
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Recombinant avian interferon-gamma (IFN-.gamma.)
Patent: US 6083724-A 1 04-JUL-2006;
                                                                                                                                                                                                                                                                                                    1 CGGATCCACTAGTAACGGCCGCCAGTGTGGTTGGAAT 36
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Patent US 5795764-A 1 18-AUG-1998;
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API01963
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192 c 227 q
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420 c 372 g
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ILKLDGATLSLAVREDYLDNSTEAKSYKDALYKFMVDTAVLLGANSSKAEHDMKSVLR
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Submitted (22-DEC-1995) Medicine, McCill University, 3755 Cate Ste
Catherine Road, Montreal, QC H3T 182, Canada
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Lipman, M.L., Panda, D., Hennett, H.P., Henderson, J.E., Shane, E., Shen, Y., Goltzman, D. and Karapils, A.C.
Cloning of human PEX CDNA. Expression, subcellular localization, and endappedilable at Litty 3. 519: Chem. 273 (22,, 12729-13737 (1998)
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Human metalloendopeptidase homolog (PEX) MENA, complete seguence.
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Pred. No. 8.8e-07;
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/protein_id="AAC24487.1"
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/db_xref="taxon:9506"
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Testa,J.E., Quigley,J.P. and Seandel,M.
Monoclonal antibodies that recognize antiqens associated with tumor
metastasis
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae, Murinae;
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Goodle Rothberg, B.E.
Wethod of ldentilying ligands for the peroxisome proliferator
activated receptor gamma using differential quue expression
Patent: WO 0144512-A 57 21-JUN-2001;
Curagen Corporation (US)
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/db_xref="taxon:10116"
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168 3 253 c 262 q 187 t
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July 15, 2003, 23-55:37 ; Search time 4167 Seconds (Without alignments) 12091.233 Million cell updates/sec Pur on:

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Scoring table:

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16154066 seqs, 8097743376 residues Searched.

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ALIGNMENTS

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RESULT 1 BI389779 LOCUS DEFINITION	ACCESSION VERSTON KEYWORDS	SOURCE ORGANISM	FFFFFFNÇE AUTHOPS TITLE JOURNAL	COMMENT	FEATHFES SOUTCE

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                                                                TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                           COMMENT
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                                                                                                                                                                                                                                                                                                    EST 15-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL449724 Homo saptens tetal brain (Stavrides GS) Homo sapiens cDNA,
                                                                                                                                                                               /tissue_type="Pituitary Gland/Rypothalamus/Pinedl Gland" "/dev_stage="Embryonic" (d12,d14,d10); post-hatch (w1,w3,w3,w9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ### HITTELLE | HITTELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Primary Chicken Piruitary/Hyporhalamus/Pineal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 GGTTGCAAGSSSTACTTCTCCCAAATSSCCCAASSATSCACAATAGSSSSACACTAAAT - 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Z72 ANABOGATGATHIGANGGATEGAATGATGATGATTGATGATTTABABATGGTGAAG 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              332 TITACTACAGAAGTAAGTACCTCCGAAGTGACATATAGAAGTATATAGAAGCAAACC 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 ITTACTACAGAAGTAAGTAPPTFPGGAAGTGAPATADAAPHGGAATATAGAAGCAAAPG + 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             452 CCAACGCATTCTCAIALIAICIGAGAGATIGTGAGTTGAGAATTATTATTA 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    512 ACATTATGAAAAPTGGGGATGATTATTATGCTACCAGACTTGAGTTGATGAGAAAA 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  572 TTGATCCACAGACTCTGGAGACACTAGATAAGGTAGACTACAGCAAATATGTAGCTGTAA 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.8%; Score 586; DB 13; Length 661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       632 ACTIGGGAACTIGTGACCCACACIALGACACIGGTGGAAATATICE 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
/strain="commercial broiler chicken"
/db_xret="taxon-9031"
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                                                                                                                                                                                                                                                                     /lab_host-"E. Coli EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 0%; Prod w.
                                                          /clone-"pgplc pk002 ala"
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                                                                                                                                                      /sex-"Male and Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL449724.1 GI:11181358
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Al.449724
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AL449724
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AJ133823 197 hp mPNA linear EST 30-APF-1999
AJ133823 Homo sapiens library (Spurkland A) Homo sapiens cDNA clone
AKK-12-35-1-1, mRNA sequence.
                                                                                 The Sanger Centre
Welledme Frust Genemae Campus, Hiexton, Camberidaeshite, CRIO 18A, UK
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 197)
                                                                                                                                                                                                                                                                                                                          /note-"cDNA fragment isolated using a cPNA end rescue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                /clone_lib="Homo sapiens tetal brain (Stavrides GS)"
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Stavildes, G.S., Huckle, F.J. and Deloukas, P.
Unpublished, Stavrides, G.S., Huckle, E.J. and Deloukas, P.
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Krist-ffrsen,A K., Spurkland,A. and Brinchmann,J.E.
STT (Kristoffersen, Spurkland, Brinchmann)
Unpublished (1999)
Contact: Spurkland A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 197;
                                                                                                                                                                                                                                                                                                                                                                                                                        1.2%; Score 36; DB 9; Length 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CGGATCCACTAGTAACGGCCCACTGTGTGTGTGTAAT
                                                                                                                    Fmail: hquqquery=sanqer.acluk
Sanqer Centre name : sced1020.t7.21p.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                               /organism:"Homo sapiens"
/db_xref-"taxon:9606"
/map="20"
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Similar sequence: M28879.
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/db_xret-"taxon:9606"
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                                                                                                                                                                                                                                                                                   /tissue_type="Brain"
/dev_stage="fetal"
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                                                              Contact: Stavrides GS
                                                                                                                                                                                                                                                                                                                                             technique"
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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EST UB MAR 2002
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                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml, Mammalia; Eutheria, Pilmates, Catairhini; Hominidae; Homo.

1 (bases 1 to 269)
Wirtz, M.K., Samples, J.R., Xu, H., Severson, T. and Acott, T.S.
Expression Profile and Genome Location of CPNA Clones from an Infant Human Trabecular Meshwork Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vērtebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini, Hominidae, Homo.
PMRR7642
TM286 Human Traberular Meshwork obna library Homo sapiens chunchone 107812 5', mRna sequence.
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HFLEST-742 Human fetal live! (S.Xue) Homo sapiens cionA, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib-"Human Trabecular Meshwork cDNA library"
                                                                                                                                                                                                                                                                                                               Oregon Health Sciences University
3375 S.W. Terwilliger Blvd., Portland, OF 97201-4197, USA
Tel: 503 494-4698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiems"
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                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop. 240.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
/clone="107812"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="eye"
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Dept of Cellular Biclogy
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Best Local Similarity 100.0%; P.
                                                                           HM887692.1 CI:19271421
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                                                                                                                                                                                                                                                                                                                                                                                         Email: wirtzm@ohsu.edu
                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: T7 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA514191.1 GI:2253715
                                                                                                                                                                                                                                                                             Contact: Wirtz MK
Glaucoma Genetics Lab
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/clone_lib="NEGGOOD"
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/note="Vector: public Site_1: Noti, Site_2: EcuRl, The CDNA library was constructed from poly(A). RNA of an adult mouse thymus by oligo-dT primed reverse transcription. CDNA was selected on yell thus size above 800 nuclections after second strand synthesis, then directionally cloned after adaptor ligation and restriction engine cleavage into the pcDNAI vector (Not I on polyA side, EcoR i on the 5'side)."
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Biology, Moscow, Russia (V Zakhariev)
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5 Deng Dan San Tiao, Beijing, 109005 P.R. China
                                                                                                                                                                          /db_xref="taxon:9606"
/cione_lib="Human fetal liver (S.Xue)"
                  Tel: MECL-55240459
Fax: %610-65240520
Bmail: Xuesp@cdm.imicams.ac.cn
Seq primer. Ml3 Forward and Reverse Primer.
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/dev_stage="fetal"
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Score 35; DB 14; Length 418;

Query Match

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Spermatophyta; Magnollophyta: endionylodons, one endiosts,
Rosidae; eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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Fax: 612 625 9728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mgM182P PFLP sequences of mungbean, Vigna radiata Vigna radiata genomic, DNA sequence.
AZ254240
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Sequence of mapped RFLP marker mgM182 on linkage group 1 of
mungbean: linkage group II of cowpea. For more information, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref-"taxon:157791"
/clone_lib*"RFLP sequences of munghean, Vigna radiata"
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/note="Vector: pUC 18; Site_1. Pst i, DNA was digested
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Menancio-Hautea, D., Kumar, L. and Young, N. D.
RFLP sequences of mungbean, Vigna radiata
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                                                                                                                                                                                   1 CGGATCCACTAGTGGGGCGGCAGTGTGGTGGAAT 36
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Pred. No. 0;
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Department of Plant Pathology
University of Minnesota
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100.08;
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Matches 86; Conservative
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Wellcome list Genome Campus, Hinxton, Cambridgeshire, Chiu isA, UK
Email, humquery-banger.ar.uk
Sanger Centre name : seed1019.t7.2fp.
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AL449722 Nome Sapiens fetal brain (Starrides 33) Home Sapiens cons.
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Budaryola, McLaboa, Chordata, Charlata, Vertebrata, Enteleostomi;
Mammalia, Eutheria, Frimates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 451)
Stavrides, G.S., Huckle, E.J. and Peloukas, P.
Unpublished, Stavrides, G.S., Huckle, E.J., and Peloukas, P.
Unpublished (2000)
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AuderSon. 0. A. Appels, R., Bailey, F., Hiake, I., Close, T., Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustalson, P., Hermann, P. G., Holton, T., Jacquemin, J.M., Jia, J., Joudiner, P., Lazo, G. R., Lin, J.J., McGuire, P., Oqihara, Y., Perchioni, N., Qualset, C., Schuch, W., Selvara), G., Sharitlou, M., Marburton, M. and Wenzel, G., Sharitlou, M., Sorrells, M., Warburton, M. and Wenzel, G., Sharitlou, M., Expressed Sequence lags for Species of the Triticeae
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MMIGO2 AGEFGGGAG ITEC MWI WHEAT FOOT LIBEATY Trifferm ACKLIGHM CDNA CLODE MWLO02.AGE, mRNA SEQUENCE.
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/dev_stage="fetal"
/note="cDNA fragment isolated using a cDNA end rescue
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International Triticeae EST Cooperative (ITEC)
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Contact: Warburton M
Applied Biotechnology Center, CIMMYT
Apdo Postal 6-641, 06600 Mexico DF MEXICO
Fax: 52-5-7269091 ext 1381
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/db_xref="taxon:9606"
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Acquence of mapped RFLP marker mgQ117 on linkage group 4 of mangled RFLP marker mgQ117 on linkage group 4 of mangled RFLP more information, see BeanGenes at:

http://drs.grn.mn-.orto-li-chip.pi-lin/Weilary.w-lear-db-beangenesscl ass=Locus. Please see as authorities for mapping/maming: Patokun, C.A., Danesh, D., Young, N.D. (1993) RFLP linkage map for cowpea (Vigna unguiculata (L.) Walp.) in: Genetic Maps, 1992. S. J. O'Brien, ed. Cold Spring Harbor Press, Cold Spring Harbor NV, pp. 6.259-6.260.
                                         Eukaryota, Viridipiantae, Streptephyta, Embryophyta, Tracheophyta;
Spermatophyta; Magnollophyta; eudlootyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                    495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul MN 55108, USA
Ici. 612 625 2225
Fax: 612 625 9728
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1 (bases 1 to 503)
19, 2. He,F. and Xue,S.
Human liver ESTS
Unpublished (1997)
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/dev_stage="Sprouts"
/intu="Vectur: pUT 18: Site_1: Fst 1; DHA was digested
with Pst 1 site separated by sucrose gradient
centrifugation and the fraction between 500:5000 base
pairs ligated into the vector using standard method."
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/clone_lib="RFLP sequences of mungbean, Vigna radiata"
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HFLEST-741 Human fetal liver (S.Xue) Homo sapiens CDNA, mRNA
                                                                                                                                                  Denny, R., Danesh, D., Mudge, J., Ccoper, A., Larson, K., Menancio: Hautea, D., Kumar, L. and Young, N.D. MFLP sequences of mungbean, Vigna radiata Unpublished (2000)
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                                                                                                                                                                                                                                       Contact: Young Nevin D
Department of Flant Pathology
University of Minnesota
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                                                                                                                                                                                                                                                                                                                                                                       Email: neviny@tc.umn.edu
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Class: RFLP probe.
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Rosidae; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MC28R Apple cDNA Library Malus x domestica cDNA clone MC28, mRNA sequence.
                                                                                                                                                                                  /dev_stage="8 day old"
/note="Vector: pYES2 (Invitrogen); 0.5-1.5 Kbp average insert size."
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                                                                                                                           /clone="MWL002.A06"
/clone_lib="ITEC MWL Wheat Root Library"
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Craziano,E. and Arus,P.
Sequences of RFLP mapped cDNAs in Prunus
(inpublished (2001)
Contart: Graziano E
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                                                             /organism="Triticum aestivum"
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http://wheat.pw usda gev/genome
                                                                                  /cultivar="Atlas"
/db_xref="taxon:4565"
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EST 14-JUL-1997

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/note-"Vector: pcDNA1; Site_1: Not1; Site_2: EcoR1; The
cDNA library was constructed from poly(A)+ RNA of an adult
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                 Institute of Hasic Medical sciences/Peking Union Medical College & Chinese Academy of Medical Sciences(FDMC & CAMS)
5 Dong Dan San Tiao, Reijing, 100008 P. China
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 555)
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/clone-"MTA.C02.079"
/clone_lib-"MTA adult mouse thymus library"
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/cloue_ilb="Hummn letal liver (s.Xue)"
/tissuc_type="liver"
/dev_stage="fetal"
/lab_host="E.coli DH5a"
                                                                                                                   Email: Xuesp@cdm.imicams.ac.cn
Seq primer: Ml3 Forward and Reverse Primer
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Tel: 330491269496
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Contact: Jordan BR
Genome Structure and Immune Functions
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tive 0; Mismatches
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Dept of Cellular Biology
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                                                                          Tel: 8601-65296459
Fax: 8610-65240529
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ORIGIN

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Anote—"Vector: pcDNA4; Site_1: EcoRI; Site_2: EcoRI; Human cdNA library made from mRNA isolated from trabecular meshwork cells established fom eyes from 6 individuals, ages 2 weeks to 2 years, Cells were harvested at passages 3 through 6. Invitroera made a unidirectional coNA library from the mRNA from the frozen cells using a pcDNA4 vector and TPDIOF" host cells."
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1 (bases 1 to 612)

Wirtz M K Samples, 1 F Xu. H , Severson, T. and Acott, T.S. Expression Profile and Genome Location of cDNA Clones from an Infant Human Trabecular Meshwork Library

Contact: Wirtz M Glaucoma Genetics Lab
                                                                                                                                                                                                                                                                                           BMBBB419 EST 0H MAK TM077 Human Trabecular Meshwork cDNA library Homo sapiens cDNA clone 104138 5', mRNA sequence.
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/clone_lib="Human Trabecular Meshwork cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oregon Health Sciences University
3375 S.W. Terwilliger Blvd., Portland, OR 97201-4197, USA
Tel: 503-494-4698
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1.2%; Score 36; DB 14; Length 555;
100 0%; Prod No 0;
tive 0; Mismatches 0; Indels
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                                                                                                           1 CGGATCCACTAGTAACGGCCGCCAGTGTGGTGGAAT 36
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/cell_type="trabecular meshwork"
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/db_xref="taxon:9606"
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High quality sequence stop: 350.
Location/Qualifiers
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SM Homo sapiens
Eukaryota, Medata, Chardata; Chariata, Vertubrata, Eutuleostomi,
Mammalia; Futheria; Primates; Catarrhini; Homanidae; Homo.
Mammalia; Futheria; Primates; Catarrhini; Homanidae; Homo.
I (bases 1 to 633)
Wirtz,M.K., Samples,J.R., Xu,H., Severson,T. and Acott,T.S.
Expression Profile and Genome Location of CDNA Clones from an Infant Human Trabecular Meshwork Library
Contact: Wirtz MK
Glaucoma Genetics Lab
Oregon Health Sciences University
3375 S.W. Ferwilliger Blvd., Portland, OR 97201-4197, USA
Tel: 503-494-4685
Eax: 503-494-6875
Email: wirtzmichsusedu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONT. Stre_1: ECORI; Site_1: ECORI; Human cdNA library made from mRNA isolated from trabecular meshwork cells established fom eyes from 6 individuals, ages 2 weeks to 2 years. Cells were harvested at passages 3 through 6. Invitrogen made a unidirectional cDNA library from the mRNA from the frozen cells using a pcDNA3 vector and PPO10F' host cells."

3 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/clone_lib="Human Trabecular Meshwork cDNA library"
/tissue_type="eye"
/cell_type="trabecular meshwork"
/dcv_slage "2 week to 2 year old infants"
/lab_host="TOP10F""
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1.2%; Score 36; DB 14; Length 633;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 36; Conservative 0; Mismatches 0; Indels
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Job time : 4170 secs
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AUTHORS
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GenCore version 5 1.6
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OM nucleic - nucleic search, using sw model

(without alignments) 10066.095 Million cell updates/sec July 16, 2003, 00:14:52 , Search *ime 488 Seconds Pun on-

adadananananananananan 3111 1 eggatecaetagtaaeggee. US-10-053-192-2 3111 Perfect score: Sequence:

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1105431 seqs, 789497551 residues Searched.

Ô Word size : Total number of hits satisfying chosen parameters:

Minimum DB seq length։ 0 Maximum DB seq length։ 2նասարդիրը

Post-processing: Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

bescription	Sequence 2, Appli	Stratefine C. App. 1	Sequence 116, App	Sequence 89, Appl	Sequence 1, Appli	Sequence 112, App	Symptopic 2577. Apr	Sequence 6573, Ap	Sequence 712, App	Sequence 11, Appl	Sequence 67. Appl	Sequence 2945, Ap	Sequence 3008, Ap	Sequence 2945, Ap	Sequence tode, Ap	Sequence 16, Appl	ų,	17	
1.0	US-10-053-192-2	US-10 201-386-6	115-04-433-747-116	US-09-933-797-89	US-09-443-218-1	118-00-033-797-112	113-09-796-692-6673	US-10-040-862-6573	US-09-834-975-712	US-09-900-530A-11	DS-09 864-864-67	118-09-746-692-2945	115-69-7967-60-3m	115-10-040-862-2945	US-10-040-862 0005	115-10-043-881-16	115-09-017-176-16	115-09-765-780A-17	US-09-765-870-17
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Sequence 15, Appl Sequence 15, Appl	Sequence 16, Appl	Sequence 16, Appl	Sequence 1515, Ap	Sequence 207, App	Sequence 33, Appl	Sequence 1182, Ap			Sequence 1282, Ap	217,	Sequence 223, App	Sequence 32, Appl	Sequence 211, App	Sequence 18, Appl	Sequence 183, App	Sequence 3745, Ap	Sequence 3745, Ap	Sequence 1807, Ap	Sequence 2953, Ap	Sequence 2953, Ap	Sorpresson 1240, Ap	Sequence 1240, Ap	Sequence 1240, Ap	Sequence 1240, Ap
US-10-043-881-15	US 09 765 780A 15	118-09-765-870-16	115-09-815-343-1515	US-09-815-343-207	US-09-911-781-33	118 - 0 - 4 - 4 - 4 - 5 - 5 - 5 - 5 - 5 - 5 - 5	US+0a+902+a41-1782	US-02-844-626-1282	US:10:017:754:1282	US 09-815 343 217	US 09:815:343 223	US-10-035-098-32	US-09-815-343-211	US-10-115-278-18	US-10-066-543-183	US-09-796-692-3745	US-10-040-862-3745	US-10-102-524-18C7	US-U9-796-692 2953	US-10-040-862-2953	13 03-7 46 457 1240	US-09-902-941-1240	US-09-849-626-1240	PS-10-017-754-1240
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TITLE OF INVENTION. BEJORNES COONED THEREOR AND THEIR USE
FILE REFERENCE: B, B-CAROTENE 15, 15'-DIOXYGENASES, NUCLEIC ACID
FILE REFERENCE: B, B-CAROTENE 15, 15'-DIOXYGENASES, ...
CUPPENT APPLICALIAN NUMBER 15, 15'-DIOXYGENASES, ...
CUPPENT APPLICALIAN NUMBER 105, 15'-DIOXYGENASES, ...
CUPPENT APPLICALIAN NUMBER 105, 10, 202-01-15.
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PRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 10
                                                          , Sequence 2, Application USZ10052192
: Publication No. USZ1023U87336Al
: GENEPAL INFORMATION:
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Db	1381	AAGTATGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
Qy	1441	ABIGICCAAA?AAAGAAAGTATGAA;GAAAAAAAAAAAATGCIGGCCCCAAAAAAAAAAAAAAAAA
QQ	1441	AATGTCCAAACAAAGGAAGTACTGGAGTGGAGAAGAATAGCATTGTTGGCTCACAAACCAAACAAA
Qy Db	1501	ATCTTIGTTCCAGCCCAAGCAAGAACAAGAATGAACGATGTTGTTTTTACCGGTGTGTT-1560 FILLHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTH
Qy	1561	GIGGIGICIGAGCCAAATAAAGCACCCTTCCTACTCATCTTGAGGTAAAACATTCAAA 1620
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Qy	1671	GAATTAGAAAAGAAAGITAAAATAAAAADAAAATTAAAAATAGAAATTATATA 1680
Db	1621	SAATTEGGEGGAGGAGAGTTAACGTAGAATGCATCTGGACTTGGATGGGATGTTATA 1680
Qy	1681	CCACAGAATGATTGGGGGCTGAGACGGAATAAAAGGCTATTGALCCGACTACACAAACT 1740
qq	1681	CCACAGAALGALITGGGGGGGGGGAATAAAACGCTATTGATCCGACTACAAAACT 1740
QY	1741	GAGACAACTTTCIACIGAACAIGAGIIAAIAICCCTTTTACCATTCAAAAAAAAAA
Dh	1741	GAGAÇAACTTTCTACTGAACATGAGTTAATATCCCTTTTACCATTCAASAAAAAAAATAT THUU
QY	1801	AAGGACACAAAATGACTATGTATAATGTCTTTAAATAATATAATATAATATAATCCTTTTAAGGACAC 1860
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Ōy	1861	AGGGATGAGTTTTACTAGAGGTAAGGATATGCAGAACTGGCATATAACTTATTCCAAAAGA 1920
Dh	1861	AGCGATGAGTTTTACTACGGTAACGATATGCACAACTGGCATAGACTATTCCAAAAGA 1920
Qy	1921	AGAAGAACGATCAGTGTTTTAGAAGTGCTAATGTTGTACATAACGGGGGAAAAAAAA
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ζ		GATOSTTSCAAGAFDSCAGTD COGAGGGAGTTTCTCTCGAGGGAAACCTCATTTA 2160
D.b	2101	GATCOTTTCAAGATIGCAGCTIGTGAAGGTITCLCCAGCCAGAAAACGTATIIIA 21+0
Qy	2161	AACCAPCTRCTACTAATTCATACCAATGCATTCTTGGGGTGCPCGGTTTACACTATA 2220
QQ		AACCATCTCCTACTCCTACTCATACCATCCATTTCCTCCT
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Db		ACCAMAGITAMGITIAGAITCAGGISGIACAAGITICIAATTIAGAAGIGAAGIAAAGA 2280
Qy	2281	ASCAAACAGACTEGCTATAGCTAATAACCCAAGGTATTFFFCCT11111A1GATGACA 2.440
qa		AGCAAACAGCACTTGCTTTGCTAATAACCCCATGGTGTATTTTTTCTTTTTTATGATGACA 2440
Qy	2341	AAACCAAGTACATATGGTTTTATGTAGCATTCAATTATACTTCAGTGCTATTCCATCTA 2400

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2461 GIGTAATGAGAGGAGTAGGTGGGTAAAGAGGAAGGAAGGTAGGITTAATAGTAFG 2520
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CURRENT APPLICATION NUMBER 115,10,201, 385, CURRENT FILING DATE: 2002-07-23 PRIOF PLILING DATE: 2002-03-24 PRIOF FILING DATE: 2000-03-24 PRIOF FILING DATE: 1999-11-05 PRIOF FILING DATE: 1999-11-05 PRIOF FILING DATE: 1998-02-02 PRIOF FILING DATE: 1998-02-02 PRIOF FILING DATE: 1998-02-02 PRIOF FILING DATE: 1998-02-02
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, Publication No. US20030091567A1
; GENERAL INFORMATION:
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APPLICANT: Joukov, Vladimir
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ITLE OF INVENTION: Isolation and Use of Fetal Urogenital
IILLE OF INVENTION: Sinus Expressed Sequences
FILE PEPERENNE. 9901-007-999
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Best Local Similarity 100.0%; Prod No 1 7e-0
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SOFTWARE: FastSEQ for Windows Version 3 0
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PRIOR APPLICATION NUMBER: US/09/482,933
PPIOP FILLING DAFF: 2000-01-14
PRIOR FILING DATE: 1990-08-01
PRIOR PILINGATION WINRER: 08/671,573
PRIOR FILING DATE: 1996-06-28
FELUE AFFLICATION NUMBER: 08/601,132
PRIOR PILING DATE: 1946-02-14
PRIOR PRILICATION NUMBER: 08/585,895
PRIOR FILING NATE: 1996-01-12
                                                                                                                                                             FELCE AFFLICATION NUMBER 08,510,133
PRIOR FLIMO DATE: 1995-08-01
PRIOR PELLING DATE: 1995-04-011
PRIOR FILING DATE: 1994-11-14
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Patent No. US20020155119A1
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Patent No. USconpol55119A1
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US-09-933-797-116
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Best Local Similarity
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                  APPLICANT: Robert A. Sikos et al.
TITLE OF INVENTION: Isolation and Use of Fetal Urogenital
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100.0%, Fred. No. 1.7e 07,
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FILE REFERENCE: 9901-007-999
CHRRENT APPLICATION NUMBER: US/05/53.797
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                                                                                                                             CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: US/09/482,933
PRIOR APPLICATION NUMBER: US/09/482,933
PRIOR APPLICATION NUMBER: PCT/US99/10/46
PRIOR FILING DATE: 1994-05/14
PRIOR FILING DATE: 1994-05/14
PRIOR FILING DATE: 1998-05-14
NUMBER: OF SEQ ID NOS: 811
SCOTWARE: FASISEQ for Windows Version 3.0
SEQ ID NO 899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/443,218
CURRENT FILING DATE: 1999-11-19
PRIOR APPLICATION NUMBER: US 08/755,381
PRIOR FILING DATE: 1966-12-19
PRIOR FILING DATE: 1996-03-05
PRIOR APPLICATION NUMBER: AU PNI542/95
PRIOR FILING DATE: 1995-03-06
PRIOR APPLICATION NUMBER: AU PNI542/95
PRIOR FILING DATE: 1995-03-06
PRIOR FILING DATE: 1995-03-06
NUMBER OF SEO ID NOS: 10
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LACATION: (1)...(575)
OTHER INFORMATION: n = A,T,C or G
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Publication No. US20030099610A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lowenthal, John W
APPLICANT: Johnson, Michael A
APPLICANT: O'Neil, Terri E.
APPLICANT: York, Jennier J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Gallus sp. (chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 46, Conservative
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LOCATION. (144)..(625)
NAME/KEY: mat_poptide
LOCATION: (191)..(625)
NAME/KEY: 3'TITR
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NAME/KEY: 5'UTR
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GENERAL INFORMATION:
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1.1%; Score 35; DB 9; Length 1079;

Query Match

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APPLICANT: Algate, Paul A.
APPLICANT: Mandan, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE PEREPREPREP: 2017 OUT, 2017
CURRENT APPLICATION NUMBER: 0201-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR APPLICATION UMBER: 60/186,126
PRIOR APPLICATION UMBER: 2000-03-01
PRIOR APPLICATION UMBER: 0200-03-01
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                              Indels
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TITLE OF INVENTION: ISOlation and Use of Fetal Urogenital
TITLE OF INVENTION: Sinus Expressed Sequences
FILE SEFERACE: 9001-007-999
CURRENT APPLICATION NUMBER: US/209/933,797
FILING TILING THE: 2001-01-08-22
FRICH PAPLICATION NUMBER: POINT-933
PRIOR FILING DATE: 2000-01-14
PRIOR FILING DATE: 1949-05/14
PRIOR FILING DATE: 1949-05/14
PRIOR PRIOR TILING DATE: 1949-05/14
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1.0%; Score 32; DB 9; Lc
Best Local Similarity 100.0%; Prod. No. 1.8e-05;
Matches 32; Conservative 0; Mismatches 0;
luu.0%; Pred. No. 5.9e-07;
tive 0; Mismatches 0,
                                                                                                             2 GGATCCACTAGTAGGGGGGGGGGGGTGTGGTGGAAT 36
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SOFTWAKE: FastSEQ for Windows Version 3.0
SEQ 1D NO 112
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Publication No. US20020198362A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
                                                                                                                                                                                                                                                                ; Sequence 112, Application US/09933797
; Patent No. US20020155119A1
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2000-04-27
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APPLICATION NUMBER: 60/200,779
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2000-05-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (1)...(331) ; OTHER INFORMATION: n = A,T,C or G US-09-933-797-112
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                              35; Conservative
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FRICE APPLICATION NUMBER: 6
PRIOR FILLING DATE: 2000-04-
PRIOR APPLICATION NUMBER: 6
PRIOR FILLING DATE: 2000-04-
PRIOR APPLICATION NUMBER: 6
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FILING DATE: 2000-01
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        Best Local Similarity
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                              Matches
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APPLICANT: Seol, Dae-Mu
AFFLLCANT: Billiar, ilmothy R.
TITLE OF INVENTION: DAM Cassette for the Production of
TITLE OF INVENTION. Secretable Recambinant Trimenic Trail Froteins, Tetracycline
TITLE OF INVENTION. Assorption Industrial Addition Associated Virus Vector, Their
TITLE OF INVENTION. Combination and Use in Some Therapy
FILE PEPPENCE: 5006-1-902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: BOLL, ANGRAM
APPLICANT: BOLL, ANGRAM
APPLICANT: Un Huttel, Christophe
APPLICANT: Van Huttel, Christophe
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
TITLE OF INVENTION: OF HUMAN CANCERS
TITLE OF INVENTION: OF HUMAN CANCERS
TITLE OF INVENTION: OF HUMAN CANCERS
CURRENT APPLICATION NUMBER: US/09/834,975
CURRENT APPLICATION NUMBER: E0/197,538
PRIOR PPLICALING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 1046
SOFTWARE: FASTERO FOR WINDOWS VERSION 4.0
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100 09; Pred No 0.0053;
tive 0; Mismatches 0; Indels
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Local Similarity 100.0%; Pred. No. 0.00053;
hes 29; Conservative 0; Mismatches 0;
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CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: KR 2000-38441
PRIOR PILING DATE: 2000-07-06
NUMBER OF SEQ ID NOS: 48
SOFTWARE, FASUSEG for Windows Version 4.0
SEQ ID NO 11
     SOFTWARE: FastSEW for Windows Version 3.0 SEQ ID NO 6573
LENGTH: 101
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, Sequence 712, Application US/09834975
; Patent No. US20020110815A1
                                                                                                                                                                                                                   ) OTHER INFORMATION: n=A,T,C or G
US-10-040-862-6573
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APPLICANT: Brown, Jeffrey
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                                                                                                            OFGANISM: Homo sapiens
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                                                                                                                                                                   NAME/KEY: unsure
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                                                                                      TYPE: DNA
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APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Eetection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-01352603
FILE REFERENCE: 014058-01352603
FURKEN FAPLICATION NUMBER: US/10/040,862
FURFENT FITTH: DATE: 2601-11-06
PRIOR APPLICATION NUMBER: 18 60/186,126
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PRIOF AFPLICALION NUMBEP: 56,266,201
PRIOF FILING TATE: 2000-05-72
PRIOF FILING TATE: 2000-07-14
PRIOF FILING TATE: 2000-07-14
PRIOF FILING TATE: 2000-07-14
PRIOF FILING TATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-07
NUMBER: 6/223,378
PRIOR FILING DATE: 2000-08-07
NUMBER: OF SEO ID NOS: 9597
SEO ID NO 5573
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PRIOR FILING DATE: 2003-03-17
PRIOR FILING TATE: 2000,03-17
PRIOR FILING DATE: 2000,04-27
PRIOR APPLICATION NUMBER: US 60/200,303
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PRIOP FILING DATE: 2000-05-22
PRIOP APPLICATION NUMBER: US 50/218,950
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PPIOF APPLICATION NUMBER: US 60/223,416
PRIOF FITING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: US 60/223,378
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APPLICATION NUMBER: US 60/200,779
FILING DATE: 2000-04-28
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FILING DATE: 2000-05-01
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PRIOR FILING DATE: 2000-05-04
PPIOP AFFLICATION NUMBER: US 50/206,202
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AFFLICATION NUMBER: US 60/222,963
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PRIOR FILING DATE: 2001-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 6573, Application US/10040862; Publication No. US20030078396A1; GENFRAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (101)
OTHER INFORMALLON: u=A,T,C or G
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APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
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Matches 29; Conservative
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PRIOR
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SEQ ID NO 2945
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Best Local S
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PPIOP
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APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIACHOSIS AND THEBAPY
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                                                                                                                                                   0
                                                                                                        Length 196;
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0 9%; Score 29; DB 10; Length 122;
100 0%; Pred No 0 00054,
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100.0%; Pred No. 0.00053;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Corixa Invention Disclosure Database SEQ ID NO 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0, Mismatches
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CURRENT FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 341
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Publication No. US2002019836281
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/186,126
PRIOR FILLING DATE: 2000-03-01
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PRIOR FILLING DATE: 2000-03-17
                                                                                                                                                                                                                                                                                                                                           Sequence 67, Application US/09864864
Patent No. US20020102679A1
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                                                                                                                                                                                                                                                                                                                                                                                                                             Mitcham, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Harlocker, Susan L. APPLICANT: Dillon, Davin C.
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APPLICANT: Lodes, Michael J.
APPLICANT: Algate, Paul A.
APPLICANT: Filing, Steve P.
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                                                                                                 Query Match
Best Local Similarity 100 0
Matches 29; Conservative
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                  TYPE: DNA
ORGANISM: cytomegalovirus
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LoCATION: (1)...(122)
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LENGTH: 106
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APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER
TITLE OF INVENTION: HEMALOLOGICAL MALIGNANCIES
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SOPTWARE PastSEQ for Windows Version 3.0
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PRIOR APPLICATION NUMBER: 60/200, 304
PRIOR PILING DATE: 2000-04-29
FRICR FILING DATE: 2000-04-29
FRICR FILING DATE: 2000-04-39
PRIOR PRILING DATE: 2000-09-99
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-01
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Publication No. US20020198362A1
GENERAL INFORMATION:
                                                                                                 PRIOR APPLICATION NUMBER: 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,999
                                                                                                                                                                          PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR FILING DATE: 2000-05-04
                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION WINBER: 66/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 66/2122,403
PRIOR APPLICATION NUMBER: 60/200,545
                                                  APPLICATION NUMBER: 60/200,303
FILING DATE: 2000-04-28
                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/206, 201
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PRIOR AFFLICATION NUMBER: 69/223,416
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PRIOR FILING DATE: 2000-08-07
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PRIOR APPLICATION NUMBER: 60/190,479
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PRIOR APPLICATION NUMBER: 60/200,545
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FILING DATE: 2000-08-04
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APPLICATION NUMBER: 60,206,201
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FRIOR APPLICATION NUMBER: 60/223,378
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                         FILING DATE: 2000-04-27
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29; Conservative
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; ORGANISM: Homo sapiens
US-09-796-692-2945
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US-09-796-692-3006/c
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LITLE OF INVENTION: Hematological Maignancies
FITE OF INVENTION: Hematological Maignancies
FILE REFERENCE: 014058-01352005
CUPRENT APPLICATION NUMBER- US/10/040,862
CUPRENT FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER- US 60/186,126
PRIOR ELILNG DATE: 2000-03-01
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100.0%; Pred. No. 0.00054;
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       91 033A100ACTASTAROSSOCIONICAGIGNG 63
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PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APLICATION NUMBER: US 60/200,545
PRIOR APLICATION NUMBER: US 60/200,303
PRIOR APLLICATION NUMBER: US 60/200,303
PRIOR APLLICATION NUMBER: US 60/200,303
PRIOR PLIING PATE: 2000-04-28
PRIOR PLIING PATE: 2000-04-39
PRIOR PLIING PATE: 2000-04-39
PRIOR APLLICATION NUMBER: US 60/200,094
PRIOR PLIING PATE: 2000-05-01
PRIOR AFLICATION NUMBER: US 60/202,084
PRIOR PLIING PATE: 2000-05-01
PRIOR PLIING PATE: 2000-05-03
PRIOR FILING PATE: 2000-05-03
PRIOR PLIING PATE: 2000-05-03
PRIOR PLIING PATE: 2000-08-03
PRIOR PLIING PATE: 2000-08-03
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PRIOP FILING DATE: 2009-08-07
FRICH APPLICATION NUMBER, US 29,736,692
NUMBER OF SEQ ID NOS: 10467
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                                                                                           Sequence 3006, Application US/10040862
Publication No. US20030078396A1
                                                                                                                                                                                       APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc
APPLICANT: Corixa Corporation
                                                                                                                                                    APPLICANI: Gaiger, Alexander
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Best Local Similarity
Matches 29, Conservi
                                                                                                                                 GENERAL INFORMATION:
                                                                            US-10-040-862-3006/C
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                                                              RESULT 15
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100.0%; Pred No 0.00054;
tive 0; Mismatches 0;
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PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 9597
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3006
LENGIH: 138
                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 2945, Application US/10040862; Publication No US20030078396A1
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APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
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Matches 29; Conservative
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APPLICANT:
APPLICANT:
                                                                                             TYPE: DNA
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1 CGGATCCACTAGTAACGGCCGCCAGTGTG 29

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GenCore version 5.1.5 Copyright (c) 1993 - 2003 Compugen 1+4
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OM nucleir - nucleir search, using sw model

July 15, 2003, 20:19:01; Search time 64f Seconds (without alignments) 10861.984 Million cell updates/sec Run on:

US-10-053-192-2 Title:

... sasaaaaaaaaaaaaaaaa 3111 l nggatocactagtaacggcc. Perfect score. Sequence.

Scoring table:

OLIGO_NUT Gapop 60 0 , Ganext 60.0

2185239 seqs, 1125999159 residues Searched.

C Word size : Minimum DB seq length: 0 Maximum DB seq length: 20ຕຸ000000

Total number of hits satisfying chosen parameters:

4370478

Post-processing: Listing first 45 summaries

Database

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Pred. No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Beta, Beta-caroten	Human Flt4 ligat3	Human herpes simpl	Wheat low affinity	Chicken gamma inte	Nacheutade Sequence	cDNA encoding huma	Metastasis-assecia	PPARgamma responsi
		ID	 AAA53888	AAV48407	AAX25511	AAV1U455	AAT38068	AAV23264	_	AAZ59142	AAH22658
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		Match Length DB	 3111	219	1288	148	1079	3136	3130	871	275
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		Score	 3111	35	36	36	35	34	34	33	30

Result

No.

459786

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Heta, beta-carotene 15,15'-dioxygenase protein, nucleic acids and antibodies, useful for production of vitamin A from carotene and gene
  Brugger R, Friedlein AM, Wirtz GM, Woggon W, Wyss A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       be used to transform cells, particularly plant cells, to increase their vitamin A contents (especially in fruits and vegetables) and in gene therapy of subjects who have mutated or deleted forms of the become one thus low vitamin A levels and susceptibility to developmental or ophthalmological disorders. Antibodies raised
                                                                                                                                                                                                                                                                              Beta, beta-carotene-15,15'-dioxygenase (bCDD) is used for enzymatic conversion of beta-carotene to vitamin A and for raising specific antibodies. Nucleotides encoding all or part of bCDD are useful as primers or probes for specific amplification and/or detection of the gene that encodes bCDD, for isolation of related sequences in other organisms, for determining bCDD levels in humans (to identify subjects requiring vitamin A supplementation) and for detecting mutations in the broth quare. The nucleotide encoding book may also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          against bood are used for detection/quantification of bood in
                                                                                                                                                                                         therapy of opthalmological disorders
                                                                                                                                                                                                                                      Claim 7; Page 14-15; 37pp; English.
                                                                   2000 551036/51.
                                                                                            P-PSDB; AAY97311
  Bachmann H,
                         Wyss M.
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100.0%; Score 3111; DB 21; Length 3111; 106.0%; Pred. No. 0; Sequence 3111 BP; 1005 A, 620 C, 622 G, 864 T, 0 other,

immunoassays.

241 GCAGGGA1GCAGAGAGAGAGACIAAATACAACUGG1FIGATGGCTFGGCTCTG 300 301 CTGCACATICACTICACATITAAAAHATIGAAGTITACTACAGAASTAAGIAGCICGGAAGT 360 421 GETTATFFGGAFFCGAFGCAAAAACATATFTGCCAAGGCAFTCTCATACTTATCTCACACC 480 121 CACAGGAGAGGGATGGAGACAATATTTAACAGAAACAAAGAGAGGCATCCAGAGCCCATA 180 361 GACACATACAACTGCAATATAGAAGCAAACCGAATCGTGGTGTCTGAGTTTGGAACCATG 420 GCTTATCCGGATCCATGCAAAAACALATTTGCCAAGGCATTCTCATACTTATCTCACACC 480 481 ATTOCIGAGIICACGGACAACIGOCIGAFCAACAIFATGAAAACTGGGGGATGATTAT 540 481 ATTECTICAGT TEACGGACACTECATECACATTATGAAAACTGGGGATGATTATTAT 540 1 CGGATCCACTAGIAACGGCCGCCACTGTGGGAATCCATCCTCTATGTAACAGGAAAG EU 181 AAAGCIGAGGIGAAGGIGAGTIGAGTIGGTIGGTIGGAAGGGGTACTICTGGGAAATGGG Gaps 0; 0; Indels 0; Mismatches Owery Match 100. Best Local Similarity 106. Matches 3111, Conservative 4.2.1 4 Š 3 ò 9 q 3 <u>2</u> 5 ŝ ŝ 3 င် 3 S

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QY	1081	CACGITGITITGALAFCGITGCCIACAGAGACAATAGCITGTACATATGITTA 1)	140
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Qy	1141	AAAAAACTGGACAAAGACTTTGAAGTGAACAAACATTACTCTCATCCAACCTGCAG 120	200
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Qy	1201	GGCTTTGTTGTGCCTCTGCAGTATGAGAAGATGGAGAAGTAGGTTCTAATTTAGTGAAA 120	097
qa	1201	GEOTITIGITGIGGCTCTGCAGTATGACAAGATGCAGAAGIAGGTCCTAATTTAGTCAAA 124	260
QY	1261	CTTCCAACTTCCGCAACTGCTGTAAAAGAAAAAGATGGCAGCATGTATTGTCAAACTGAA 13:	120
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ζλ	1321	ATATTATGTGAAGGGATAGAACTGACTGTGTTAACTATAATTATAAAAAAATAC 130	4B()
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Qy	1381	AAGTATGTGTATGCAACAGAAGICCAGTGGAGCCCAGTTGCTACAAAAAGATTGCAAAAACTG 144	440
QQ	1381	AAGTATGTCTTTTCTATGTATATGTTTTTTTTTTTTTTT	440
Qy	1441	AATGTGGAAAGAAAGGAAGTGGACTGGGGAGAAAGAACCACTGGTGGGCGCTGAAAGCAAAGCCCTAG	200
qa	1441	AATGTECAAACAAAGGAAGTACTGCACTGGGGAAAGACCACTGGGCCTCAGAGCCTTAG	0.05
QY	1501	ATCITISTICOCASCOCGA GRAGAGAAAAAGAATGTGATGTTGTTGTGTGTTT 156	099
qq	1501	ATCTITGITCCCASCCCGATGCAASAGAAGGATGAAGGTGTTGTTTTTGACTGTGTTT 156	260
Oy	1551	GTGGTGTGTGAAAAAAAAAAAAAAAAAAAAAAAAAAAA	079
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à a	1001 CCACAGAATGATITGGGGGGGGGGGGGGGGGGGGGGGGGG	3761
Qy	1741 GAGACAACTIICTACIGAACAIGARTIAAIATOOOTIITIITIITIITIITII 1800	Qy 2821 CALCACATANSA
QQ	1741 GAGACAACTTTCTACTGAACATGAGTTAATATCCCTTTTACCATTCAAGAACAACCATAT 1800	7887
oy Eb	1801 AACGACACAAATGACTA GTATAATCTCTTAAATAATAGATATAATCTTTTAAGGCAC 1860 	
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G Q	ACCEPTED TO THE CONTROL OF THE CONTR	2941
oy Ph	1921 AGAAGAACGATCAGTGTTTTAGAAGIGCTAATGTTGTACGTAACGGGGGGGGAACA 1980	2y 3001 CACTGGSGTCAS
oy Oy	GGAGAGAAAAGITAACAGATAITITAATAGAATATTGITGITGITGITGITGITGITGITGITGAGGGGGGGG	Oy 3061 CCATAAAATGA
g ,	981 GGAGAGAAAGGTAACGGGAATATTTAATAGAATATAGATTTCTGAGCAAATGAAGFGCAG	
cy Db	2041 IATTTATASTATSATSATSATSATSATSATSATSATTASATSTESASSASTARSATTATASA 2100 	RESULT 2 AAV48407 ID AAV48407 standard, DN
Oy Sh	CATCITICACATIONACITOTA CON ACTION A CONSACADA CONTINE	AAV48407;
2	i satostitoanaliocasoiluisaisoaasilliotonoorasaaagorgastita z	DF 14-DEC-1998 (first e
Oy.	2161 AACCATGTGGTACIGGIAAIIJAIACGAAFGYAITTTYTTGGTGGTGT GAITACACTAIA 2220 1111111111111111111111111111111111	= 4
Qy		lymph lymph Homo
ογ	1 AGCAAACAGCACIIGGITIIGGIAAIAACCCCARGGIGIAITIIIGGITIIIAIGAIGAA 234	
qq		06-A∪@-199
Qy	2341 AAACCAAGTACATAIGGTIITARSIASCATT.AAFTATGTTETTETTETTETTETTETTTI 2400 111811111111111111111111111111111111	XX
oy.	ATGTTATAAGCAATTTGTATTTAAATCAGTTTTCCTTGAGAATATCTGACATAACATTTT 	(LUDW-) LUDWIG (UYHE-) UNIV HE
00 0::	ATGTIATAAGCAAITTGTATTIAAAICAGTTTTCCTTGAGAAIATCTGACATAACATTTT 2	XX PI Alitalo K, Joukov V;
AQ QQ	2461 GTGTAARGAARGATARGATTARGATTARGAAGAGAAGAG	
oy 1	2	PT New isolated vascular PT used to develop produ PT oedema, granulocytope
20 00	524 ILAMILINIOLIANIAMINITALIAMINITALIAMINITANIAMINININININININININININININININININI	
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S &	2641 AADSABSBAGAAAACESSTAFOTAFOTAFOTAROTAFOTTABSEGEROACESPOTUS 27mm HTH HTH HTH HTH HTH HTH HTH HTH HTH HT	CC (VEGF-C). The VEGF-C CC endothelial cells and CC permeability, and att
J_{L}	2751 AEGGAZAZARRIGITASSIARGESZARATISARATARTSTOTTGARRIGITA 2760	
Dh	+-4	
ć;	2761 CTACTCACTITALELEGIANSA SANAAA MAAA HAAAANIA TI SINANTTALITALIA INDINI LIBLIG	

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VEGITTGCATGTATGAAGAATACACTGCCTAATTGTAATGTFAAAAAGT 3000
                                                                                                                  FASAACCAACCACCACCACACT COTTGCT TGCTCTGTATGACTCCCTT 2940
                                                                                                                                                                                                                                                                                                                                                                             JEGITEPS ATSTATABASAATA ACHSCCTAALICTAALGI FAAAAAGE 3000
                           ATTITOCAGGAGAGAAACAAATGAAATCACTGTCACTTACTATGGCCC 2820
                                                                                      AAZAATGOGGIIIGGIGACHIGITGAIGAIIAZATAAGAIGHIIGGAG 2880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as example of Jascalar endotherial growth factor C colymptides have activities affecting growth and are defected as cells. Permonian prowth of lymphatic ond lymphatic vessels, increasing vascular frecting myelopoicsis. The products can be used for moses, for inhibiting angiogenesis, for stimulating Levischer of presentation of the products of stimulating licoys disease. They can also be used to modulate them in glandlewing they can also be used for the of endotherial cells. They can also be used to be of the of endotherial cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thelial growth factor C; vascular endothelial cell; of cell; myelopolesis; angioyoneses; inflammation; cedema, olephantiasis; Mility's discuse; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                     GATCTAGAGCTIAAGTAAGCAGTCTGGGGTTTTCAAATGTTTATATGTT
ir endothelial growth factor polypeptide(s) -
hots for treating, e a cancers, inflammation,
benia or for wound healing or tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cleated sequence.
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trafficking of leucocytes between tissues and lymphatic vessels or to affect migration in and out of the thymus.
                                                                                                                       Gaps
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infection with HSV) with a vector containing a nucleic acid
encoding the HSV receptor renders the host cells permissive to HSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is the nucleotide sequence of B5T74 clone cDNA that codes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry and replication. In the present invention, the combination of a novel porcine cell model system which is refractory to HCV entry, along with specific HSV B5 and/or HVEM (see AAY05797) receptor proteins enables the development of assays for servening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     novel human herpes simplex virus (HSV) receptor B7774 or B5 (see AAV05796), which appears to be a type II membrane-spanning, cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiviral compounds and therapeutics. The assays are useful for detecting the ability of agents to inhibit HSV entry or spread and provide for facile high-throughput screening of compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the HSV receptor, an immunogenic polypeptide or fragments of the
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libraries, peptide libraries etc., to identify potential drug
candidates. The invention also provides a vaccine comprising
                                                                                                                                                                                                                                                                                                                                                                                                            HSV receptor; B5T74; infection; diagnosis; therapy; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human herpes simplex virus receptor BS and HVEM compositions
                                                                               Score 36; DB 19; Length 219; Pred. No. 0.00033;
                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Perez A, Subramanian G;
                                                 Sequence 219 BP; 74 A; 54 C; 52 G; 39 T; 0 other;
                                                                                                                                                     1 CGGATCCACTAGTAACGGCCGCCAGTGTGTGTGTGTGTAA 36
                                                                                                                                                                       Human herpes simplex virus receptor B5T74 cDNA.
                                                                                        100.0%: Pred. u.
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                                                                                                                                                                                                                                                                       AAX25511 standard; cDNA; 1288 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fuller AO, Li Q, Mclaren NC,
                                                                                     1.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human herpes simplex virus.
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                                                                                                                   36; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                              antiviral; assay; ds.
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                                                                                               Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09920761 A2.
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                                                                                                                                                                                                                                                                                                        AAX25511;
                                                                                   Query Match
                                                                                                                     Matches
                                                                                                                                                                                                                                       RESULT 3
                                                                                                                                                                                                                                                       AAX25511
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Sequence 1288 BP; 409 A; 237 C; 285 G; 356 T; 1 other;

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(LCT1). The present invention also describes a transquaic plant, preferably a member of the genus Brassica, comprising an expression cassette containing a plant promoter operably linked to a herorologous LCT1 polynucleotide. The LCT1 polynucleotide can be used in an expression cassette for modulating heavy metal or albeli metal uptake in a plant. The transgenic plants are useful for removing heavy metals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plant low affinity cation transporter - used for modulating heavy or
                                                                                                                                                                                                                                                                                           Wheat; low affinity cation transporter; LCII; heavy metal; alkali;
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11.2%; Score 36; DB 20; Length 1288;
00 0%; Pred No 0 00026;
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                              Indels
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                                                           1 CGGATGCACTAGTAACGGCCGCCAGTGTGCGCGAAT 36
                                                                                          18 CRATCOATTACTACOACTON ACTOR GRANT 53
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                                                                                                                                                                                                                                                              Wheat low affinity cation transporter LCT1 gene.
      100 0%; Pred H.
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137..1474
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                                                                                                                                                                      AAV10366 Standard; CDNA; 1982 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                   /product- "LCT1"
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Rest Local Similarity 100 (
Matches 36; Conservative
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04-SEP-1997;
                             Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New avian cytokine(s) and nucleic acids encoding them - useful prophylactically and therapeutically against viral and bacterial infection, and to promote weight gain in poultry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COS cells transformed with plasmid preparations from individual positive clones produced very high level of recombinant ChIFN-gamma. Recombinant ChIFN-gamma showed the same degree of heat sensitivity and pH 2 sensitivity as that shown by natural ChIFN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                             Chicken, interferon; type II interferon; avian; cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lowenthal JW, Oneil TE, Rhodes S, York JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1079 BF; 347 A; 192 C; 227 G; 313 T; 0 otner,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGATCCACTAGTAACGGCCGCCAGTGTGTGTGTT111
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                                                                                                        Chicken gamma interferon - chlFN-gamma.
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134..628
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191..625
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Matches 35; Conservative
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1. 133
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                                                                                                                                                                                                                                            Gallus gallus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-SEP-1996.
                                                                                                                                                                                                                                                                                                                                                                                     mat_peptide
                                                                                                                                                                                             poultry; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Digby MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV23264;
AAT38068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                         5'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3'UTR
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Human, PEX gene, Xp22.1, X linked hypophosphatemic rickets, estectlast, parathyreid herman, PTH, estectlast, bone breakdown, parathyroid hormone related peptide; PTHrP; metabolic bone disease; esteomalacia; esteoporosis; esteopetrosis; Paget's disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein, a phosphate regulating gene with homology to endopeptidases, suggesting that PEX might be a metalloendopeptidase. It was isolated from tumours causing oncogenous hypophosphataemia osteomalacia (OHO). Compounds which are targeted to inhibit PEX active site, identified in the method of the invention, are useful for the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hyperphosphataemia or chronic renal failure. PEX can also be used as a target for the treatment of idiopathic hypercalcuria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           o: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This is the nucleotide sequence of the recombinant human tumour PEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.1%; Score 34; DB 19; Length 3130; 100.0%, Pred. No. 0.0014;
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0.0014;
0. Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding human PEX - useful for the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Henderson JE, Karaplis AC, Lipman ML;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 GATOPAPTAGTAAPGGPPGPPGPGPPGPPGPP 46
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/product= "human PEX protein"
3147..3153
/*tag= b
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Location/Qualifiers
bus..2853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig 1A-1G; 27pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA encoding human PEX protein.
                                                                                                                                                                                                                                                                                                                                                                                                    9503-0025454
                                                                                                                                                                                                                                                                                                                                             97WO-CA00617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GOLTZ) GOLTZMAN D.
(HENDZ) HENDERSON J E.
(KARAZ) KARAPLIS A C.
(LIPMZ) LIPMAN M L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPT; 1998-193628/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shen Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PANDA D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SHEN Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Monoclonal antibody, 41-2; 50-5; antigen; tumour metastasis; Hop-3 cell; PETA-3; CD151; transmembrane 4 protein superfamily, tetraspania; cancer; angious; homangiona; arthritis; ocular necessoralarization; ds
                                                                                                                                                                                                                                                                                                                                                                                                                       Diagnosis and treatment of metabolic bone diseases e.g. osteomalacia and osteoporosis comprises determining the level of parathyroid hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                therefore bone breakdown. Parathyroid hormone related poptide (PTHFP) may also serve as a substrate for PEX. PTH and PTHFP levels can be modulated using PEX. This regulates osteoblast activity, and can be used for the treatment and diagnosis of metabolic bone diseases which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               include osteomalacia, osteoporosis, osteopetrosis or Paget's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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Pred. No. 0.0014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                             Karaplis AC, Goltzman D, Lipman ML, Henderson JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 CATCCACTAGTAACGGCCGCCAGTGTGGTGGAAT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Pred. no.
                                                      "PEX protein"
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 related peptide in a patient -
                                                                                                                                                                                                               99WO-CA00895.
                                                                                                                                                                                                                                                  98CA-2245903.
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Guert Local Similarity 100.00.
Hest Local Similarity 100.00.
                                                                       3088..3093
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                                    /*tag= a
/product=
                                                                                             /*tag= b
                604..2853
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                                                                                                                                                                                                                                                                                                                                                                WP1; 2000-293177/25.
                                                                                                                                                                                                                                                                                        (UYMC-) UNIV MCGILL.
                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAY84627.
                                                                                                                                  WO200018954-A2
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                                                                                                                                                                                                           27-SEP-1999;
                                                                                                                                                                                                                                                  28-SEP-1998;
                                                                         polyA_signal
                                                                                                                                                                        06-APR-2000
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50-6 that recognize antigens associated with tumour metastasis. MAD 50-6 was used to isolate its binding antigen. This sequence represents the cloue whose expression product binds the MAD 50 6. The clone was isolated from a Hep-3 cell cDNA expression library screened with MAD 50 6. The ending sequence was shown to have homelogy to the PFIA-yClD3 quene which encodes a member of the transmerance 4 protein superfamily, also known as terraspanins. The antibodies can be used for diamonship and treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 metastatic cancers. The antibodies can also be used for treating aberrant.
PETA-3-dependent anglogenesis, e.g. in patients with hemanglomas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antibodies which recognize antiqens associated with tumor metastasis, used to develop products for the diagnosis and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a govel monoclonal antibodies (MAD) 41 2 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peroxisome proliferator activated receptor gamma; PPARgamma; HEPATO;
liter; N.(2.benzogiphenyl)-L.tyrosine; liqand; antidiabetic; NIDDM;
gene therapy; noninsulin dependent diabetes mellitus; jaundice;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.1%; Score 33; DB 21; Length 871; Local Similarity | 10 0%; Pred No 0.004; less 33; Conservative 0; Mismatature.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 871 RF: 167 A; 252 C; 263 G; 189 F; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 ATITIANTARTANTHANNANIANTHANTART 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATCCACTAGFAACGCCCCCACTGIGGTGGAAT 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arthritis, or ocular neovascularization.
                                                                                                                                                                                                                                                                                            (TYNY ) UNIV NEW YORK STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                         Seandel M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Fig 1A; 94pp; English.
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                                                                                                                         99WO-11513480
                                                                                                                                                                                          98US-0089226
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                                                                                                                                                                                                                                                                                                                                                     Quiqley JF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ammonia toxicity; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   metastatic cancers
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W. 1445 - A. 1.
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                                                                                                                                                                                                                            20-NOV-1998;
                                                                                                                         15-JUN-1999;
                                                                                                                                                                                          15-JUN-1998;
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                                                            23-DEC-1999
                                                                                                                                                                                                                                                                                                                                                         Testa JE,
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Gaps

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The invention relates to methods of identifying ligands for peroxisome proliferator activated receptor gamma (PPARgamma) using differential gene expension and also provided are PPARgamma responsive nucleotide sequences selected from HEPATO:1-18 and 44 our their complements HEPATO are nucleic acid sequences differentially expressed in layer lissues of animals following exposure to N-(2-hemosylphenyl)-L-tyrosine, a synthetic PPARgamma ligand. The methods are useful for identifying a ligand for PPARgamma and a candidate therapeutic agent for a pathophysiology associated with a PPARgamma mediated metabolic pathway, such as noninsulin-dependent diabetes mellitus (NiLDM). The information is also useful for diagnosing or determining susceptibility to a PPARgamma mediated pathophysiology e.g. NIDDM, liver failure, jaundice or ammonia mediated pathophysiology e.g. NIDDM, liver failure, jaundice or ammonia totterfling HEPATO sequences and for amplifying HEPATO sequences. HEPATO sequences and for amplifying HEPATO sequences.
                                                                                      Identifying ligands for peroxisome proliferator activated receptor gamma using differential exp.ession of genes expressed in liver tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peroxisome proliferator activated receptor gamma; PPARgamma; HEPATO; Livor; N. (2 benevylphen;1) & tyrosine, itgand anti-diabetic, NITHM, gene therapy, nonlinauith-dependent diabetes mellitus; jaundice; ammonia toxicity; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying ligands for peroxisome proliferator activated receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1,0%; Score 30; 146-23; Length 175;
100-0%; Pred. No. 0-067;
ive 0: Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 275 BF, 62 A, 74 C, 79 G, 57 T, 3 other:
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Matches 30; Conservative 0; Mismatches
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                                                                                                                                                                   Disclosure; Page 19; 84pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid sequences.
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                                                     WPI; 2001-398172/42
                   Gould-Rothberg BE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gould-Rutliberg BE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
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The invention relates to methods of identifying ligands for peroxisome expression. Also provided are perpendicularly administrated activated receptor gamma (Pephgamma) with although definition and so provided are pepagamma responsive nucleotide sequences selected from HEPATO:1-18 and 44 or their complements. HEPATO are nucleic acid sequences differentially expressed in liver fissues of animals following exposure to N.(2-benoylepheny) L.L.Cosine, a synthetic PPAKgamma and a candidate therapeutic agent for a pathophysiology associated with a PPAKgamma enables candidate therapeutic agent for a pathophysiology sociated with a PPAKgamma mediated metabolic pathway, such as noningulin-dependent diabetes mellitus (NIDDM). The invention is also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, cytokine, cell preliferation, cell differentiation, gene therapy; vacchie; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                              mediated pathophysiology e.g. NIDDM, liver failure, jaundice or ammonia toxinity HEPATO sequences are useful for constructing probes for detecting HEPATO KNA sequences and for amplifying HEPATO sequences.
gamma using differential expression of genes expressed in liver tissue
                                                                                                                                                                                                                                                                                                                                                                                            HEPATO protein or its fragments is useful as an immunogen to generate on thodies that hind HEPATO Sequences AAHLLAGLES Fepresent HEPATO
                                                                                                                                                                                                                                                                                                          useful for diagnosing or determining susceptibility to a PPARgamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated nucleic acids and polypeptides, useful for preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    where Match (0), Solve 30, 58.22, Length 355, Rest Local Similarity lugger, Prod. No. 0.065, Marches 30, Conservative 0; Mismatches 0; Indexs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 4058; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 355 RP, 71 A, 103 C, 110 G, 69 T, 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HITHITHITHITHITHITHITHITHITHITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (Costa For Act 1431 AACHS of Costs CAST (Cost 30)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human polynucleotide SEQ ID NO 4058.
                                                           Disclosure, Page 19; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA183998 standard; cDNA; 426 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tang YI, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2001; 2001WO-US04927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-MAY-2000; 20000S-0577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 FEB 2003, 2000MS OF15126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPT: 2001-514839756.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAO04067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W1230164835-AD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA183998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
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The invention relates to human polynucleotides (AAI79541-AAI93841) and the encoded proteins (AAA000010-AA01940) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The production and polymetries are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are vacious cytokine-like activities, v.q. stem cell growth lactor activity, haematopoiesis regulating activity and may be useful in the diagnosis and/or trequiment of vancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         used for detection, diagnosts and druq screening. The protein can also be used to freat inflammation of diseases including viral, bacterial, or fundal infections, allergic responses, mechanical injury associated with trainma, hereditary diseases, lymphosis or earchinga, or other conditions which activate the quies of lymphoid or neutronal tissues it can also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Endothelial differentiation gone receptor handlegen human, HFD, EDG 6; detection; diagnosis; drug screening; treatment; inflammation; disease; viral; baccerial; fungal infection; allergic response; injury; hereditary disease, lymphoma, carelinoma, lymphoid; neutonal; cascade; lymphocyte traffickling; leukscyte traffickling; leukscyte traffickling; leukscyte traffickling; signal transduction, rheumatoid synovium; autoimmune disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence encodes a movel human endothelial differentiation gone (EDG)-6 receptor homologue designated HFDG. The encoded protein can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated human endothelial differentiation gene-6 receptor homologue - used to develop products for treating or grinfertions, altergic responses, trauma, hereditary diseases, lymphoma, carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ü;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 30; DB 22; Length 426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 426 BP; 172 A; 60 C; 113 G; 65 T; 16 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.05/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3082 CTCCATAATAAAAAAAAAAAAAAAAAAA 3111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 CTCCATAATAAAAAAAAAAAAAAAAAAAAA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ALLX ) ALLELIX BIOPHARMACEUTICALS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure: Fig 2; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV69433 standard; cDNA; 1889 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98WO-CA00487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Munroe DG, Vyas TB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human edg-6 cDNA #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
es 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WP1; 1999-070147,06
                                                                                                                                                                                                                                                                                                                                                                                                               intlammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09853062-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-MAY-1498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 - MAY - 1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 Nov 1958.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV69433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Onery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
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used for treating problems involving excessive lymphocyte and leukocyte trafficking. Inhibitors of HEDS are useful for controlling signal transduction and signalling cascades in reals of the theomatoid synovium. The protein can also be used for treating autoimmune disorders such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is a gene fragment of Mycobacterium tuherculosis Cupper, line Superoxide dismutase, Cu., Luscub, Superoxide dismutase catalyses the conversion of superoxide radicals, which are mutaquite, into molecular oxyqun and hydroqun pertoxide. Cu. Lasob is thought to be important for bacterial survival in macrophages. Macrophages equal bacteria, and set about destroying them by generating superoxide radicals. The bacterium counterests by releasing sub-roxide radicals. The present seaguence is added to the truncated of Lasoft coding sequence, (AAAAAAAA) to produce a lile-length version.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           infection in animals, and for detecting the presence of Mycobacterium tubercolosis. The antibodies are also used to isolate the Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence was then added downstream of the Lys codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibodies can be developed which bind specifically to the full length protein. The antibodies are useful for detecting tuberculosis
                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel monoclonal antibodies targeted to Mycobacterium Tuberculosis superoxide dismutase, useful for detecting tuberculosis infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M. tuberculosis Cu, Zn Superoxide dismutase, SOD, gene traqment.
                                                                                                                                                                                       ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cu, In superoxide dismutase; antibody: tuberculosis; enzyme; superoxide radical; macrophage; sodC; bacterium detection; ds.
                                                                                                                                                     Score 30; DB 20; Length 1889;
Pred. No. 0.052;
                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21; Length 48;
0.2;
                                                                                                              Sequence 1889 BF; 300 A; 575 C; 537 G; 416 T; 1 of her;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 48 BP; 10 A; 15 C; 13 G; 10 T; 0 other;
                                                                                                                                                               luulu%; Prea. a...
                                                                                                                                                                                                                              1 CGGAICCACIAGIAACGGCCGCCAGIGIGG 40
                                                                                                                                                                                                                                                                 50 CGGATCCACTAGTAACGCCCCCCCAGTGTGC
                                                                                                                                                                                                                                                  Score 29:
Pred No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (YUNG-) YUNG SHIN PHARM IND CO LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 14; 28pp; English.
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                                                                                                                                                                                                                                                                                                                                                              AAA (0 40) Standard; DNA; 48 BP.
                                                                                                                                                     1.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0108309.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                     11-SEP-2000 (first entry)
                                                                                                                                                                         Rest Local Similarity 100.
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tuberculosis Cu, Zn SOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-38/619/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rest Local Similarity
                                                                              myasthenia gravis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAY96264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200029017-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wu CH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15557 - A. N. - 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                               AAA30308;
                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lee FS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        codon.
                                                                                                                                                                                                                                                                                                                                              AAA30308/C
                                                                                                                                                                                                                                                                                                                         RESULT 13
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Search completed: July 16, 2003, 00:14:45 Job time: 647 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (b) a non-antibiotic-resident selective marker and its promoter sequence. The lactic acid bacterium shuttle vector can be used as a DNA vacchne carrier, in selecting transformed cells, drugs and foods. The present sequence is that of a multiple cloning site of one of the LAB shuttle vectors of the invention.
                                                                                                                                                                                                                                                                                                                                                                       comprises a nucleic ucid sequence encoding a protein related to replication of the LAB plasmid and a non-antibiotic-resistant selective
                                                                                                                                                                                                                                                                                                                                                            A lactic acid bacterium shuttle vector useful as a DNA vaccine carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  replication and a nucleic acid sequence encoding a protein related to
                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a lactic acid bacterium (LAR) shuttle vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
  * Tr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAB plasmid sequence containing the pins starting point of
                                                                                                                                                         LAB shuttle vector multiple cloning site sequence SEQ ID No 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.9%; Score 29; DB 24; Length 49;
100 0%; Pred No 0 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
 Indela
                                                                                                                                                                             Lactic acid bacteria; Shuttle vector; LAB; DNA vargine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 49 BP; 10 A; 14 C; 14 G; 11 T; 0 other;
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                               1 CGGATCCATTACTAACGGCCGCCACTGTG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 COGATOTACTAGTAANGGOOGGAGTGTG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           replication of the LAB plasmid; and
                                                                                                                                                                                                                                                                                                                                                                                                                Example 5, Fig 4, 24pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,>>.
100 0%; Pre
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                                                                                                                                                                                                                                                                                                                    (ANAR-) ANARATA BIOTECH CORP
                                                                                                                                                                                                                                                                          09 MAR-2001; 2001JP-0067675
                                                                                                                                                                                                                                                                                              26-MAY-2000; 2000TW-0110215
                                                                                            ABA97964 standard; DNA; 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46
                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                         multiple cloning site; ds
29, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ89695 standard; DNA;
                                                                                                                                                                                                                                                                                                                                        WPI, 2002-135978/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                JP2001340090-A.
                                                                                                                                     25-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07 - NOV - 1995
                                                                                                                                                                                                                                                     11-DEC-2001.
                                                                                                                                                                                                             Synthetic.
                                                                                                               ABA97964:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ89695;
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 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
                                                                       RESULT 14
                                                                                  ABA97964
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A universal vector complises a PL promoter, a ribosome binding site, the first 30 th of the dalta-7 pig sometastatin gate, a 21 bp frontend oligonuclectide (pref. the dimer comprising the complementary stradus given in AARCF052 Strangs and complementary maltage to comprising the strands given in AAARCF0556; containing at least 1 restriction enzyme site, a transcription terminator (pref. the dimer comprising the strands given in AAARSF05756) containing at least 1 restriction enzyme site, a transcription terminator (pref. the dimer comprising the strands given in AAARSF057758) and a drug resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Universal cloning vector for expression of heterologous genes or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - allows high levels of expression without the need for
Whiversal cloning vector, grie expression, efnNA expression, back-end oligonucleotide, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.9%; Score 29; DB 16; Length 94;
100.0%; Pred. No. 0.19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 94 BF, 20 A, 20 C, 28 G, 20 I, 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synenki RM, Zook CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; P. P. C. A. C. A. Watlve 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 9; Fig. 3; 40pp; English.
                                                                                                                                                                                                                                                                                       94WO-US11719.
                                                                                                                                                                                                                                                                                                                                                       9311S-0134148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence modification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1995-161805/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McMullen JR,
                                                                                                                                                                                                                                                                                   14-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                       15-OCT-1993;
                                                                                                                                                          WO9510620-A.
                                                                                                                                                                                                                          20-APR-1995.
                                                                                              Synthetic.
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

July 16, 2003, 00 03 57, Search time 147 Seconds (Without alignments) 6964.025 Million cell updates/sec Run on

US-10-053-192-2 Title:

1 cygatecactagtaacggee Perfect score: :aouanbas

Scoring table:

OLIGO_NUC Gapop 60.0 , Gapext 60 0

441362 seqs, 153338381 residues

0 Word size :

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Listing first 45 summaries

Database :

Issued_Patents_NA:*

/rgn2_6/ptodata/l/ina/6A_rown seq.* /rgn2_6/ptodata/l/ina/Re_rown seq.* /rgn2_6/ptodata/l/ina/Prtig_rown seq.* /rgn2_6/ptodata/l/ina/backfiles1.seq.* /cgn2_6/ptodata/1/ina/5A_COMB seq * /cgn2_6/ptodata/1/ina/5H_COMB seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

	Description	TESTA SETTINGS		ניו	9	53	Sequence 1, Appli	1	1,	H	(۳)	75	75,	75,	7.	Sequence 17, Appl	17,	Sequence 7, Applit	16,	Sequence 16, Appl	365,	381,	46.1	Sequence 383, App	154,	Š	15, A	Sequence 15, Appl
SOMMANIES	TD	US 08-795-430-6	US:08 510-133A-25	US-08-585 895-25	355-700-	US-08 601-132-25	US-08-000-148-1	US-08-765-381-1	US-08-525 697-1	1-665-888-60-81	- 1	52.0255 757.80.51	US-08 34C-426D-75	0.5-08-450-6730-75	PCT-US95-17111A-75	US-08-604 165-17	US-08-734-054B-17	ng-00-350-361 7	11S-11H-14-165-16	TS-08 734 054B-16	US-09 404-879A-365	US-09-404-879A-381	4 (14 -	US · 09 · 404 · 879A · 383	-80-	HS-09-404-875A 233	-08 821-	11S-09-290-202R 15
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Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 24, Appl	Sequence 23, Appl	Sequence 46, Appl	Sequence 45, Appl		ις ,	٠,	'n	ά·	4,	sequence 3, Appli	Sequence 4, Appli	81,	4,	Sequence 1, Appli
US-08-616-468A-2	08+09+054+298+2	US 09 818 655 2	US-09-175-658B-24	US-09-175-659B-23	US-08-991-789A-46	itS-04-062-451-46	11.55 - 12.15 - 12.15 - 12.15 - 12.15 - 12.15 - 12.15 - 12.15	HS-04-874-027-5	11S-018-450-048-3	US-08-458-023B-3	US-09-378-088A-89	US-09-015-188-4	0.5-08-908-758-3	87 08 359 376-4	US-09-378-088A-81	45-08-008-158-4	US-04-216-909-1
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ALIGNMENTS

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APPLICANT: Joukov, Vladimir
TITLE OF INVENTION: Vascuiar Endothelial Growth Factor C (VEGE-C)
TITLE OF INVENTION: Protein and Gene, Matrits Thereof, and Uses Thereof
NUMBER OF SEQUENCES: 57
                                                                                                                                                                                                                                                             E: Marshall, O'Toole, Gerstein, Murray & Borun
blou Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
UPFRITING SYSTEM: PC-DOS/MS-LOS
SUFTWARE: ParentIN Pelease #1 0, Version #1 30
APPLICATION DATA:
APPLICATION NUMBER: US/US/195,430
FILLIGATE: NUMBER: US/US/195,430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PETEREWILLOWYKET NUMBER CHARLY 34691
TELECOMMUNICATION INFORMATION:
TELECHONE 312,474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION. 435
PRIOR APPLICATION DATA:
AFFLICATION NUMBER. FCT/F196/00427
FILING DATE: 01-AUG-1996
PRIOR APPLICATION DATA:
AFFLICATION NUMBER. 03/671,573
                                                                                                                                                                                                                                                                                                                                                        COUNTRY: United States of America ZIP: AñAŋ6-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR ARTHLAND WORBER, C8/501,132, FALLING DATE: 14 FEB-1996
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
______NTTON NIMBER: 09/510,133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08,7340,011
                                          Sequence 6, Application US/08795430
Patent No. 6130071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38,153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILLING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 28-JUN-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-ATG-1995
                                                                                                                 APPLICANT: Alitalo, Kari
APPLICANT: Joukov, Vladi
                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PETOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Gass, David A. PEGISTPATION NUMBEP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NIMBER.
                                                                                                                                                                                                                                                                                                                                      Illinois
                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                      STREET: blow S
CITY: Chicago
STATE: Illinoi
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                 US-08-795-430-6
RESULT 1
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US-08-585-895-25
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                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Warker Drive
                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSIEM: PC-LOUS/NS-(NUS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NOMER: US/08/510.133A
FILING DATE: 01-Aug-1995
CLASSIFICATION: CURROWN>
                                                                                                                                                                                                                               1.2%; Score 36; DB 3; Length 219; 100.0%; Pred. No. 2.8e·06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.2%; Score 36; DB 4; Length 219; 100 0%; Prod No 2 Ro-06; tive 0, Mismatches 6, Indels
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                                                                                                                                                                                                                                                                                                                                         1 CGGATGCACTACTAACGCCCCCACTCTCCTCGTCGAACT 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 28113/32863
TELLECOMMUNICATION: INFORMATION:
TELEPHONE: 312/474-6500
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                Hest Local Similarity 100.0%; Pred. No. 2.8
Matches 36; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: United States of America ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ 1D NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOUKOV, Vladomir
TITLE OF INVENTION Reveptor Ligand
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 38,153
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 25, Application US/08510133A
; Patent No. 6221839
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 219 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Gass, David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEG ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Alitalo, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                         SECTENCE CHARACTERISTICS:
LENGTH: 219 base pairs
TYPE: nucleic acid
               TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100
Matches 16, Conservative
112/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Illinois
                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chicago
                                                                                                                                                                 MOLECULE TYPE: CONA
                                                                                                                                               Linear
                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 2
US-08-510-133A-25
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                                                                                                                                               ropology:
  TELEFAX:
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RESULT 3

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APPLICANT, Ludwig Institute for Cancer Research
Helsinki University Licensing
Alitalo, Kari(U.S. only)
Joukov, Vladimir (U.S. only)
TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
Protein and Geno, Mutants Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET, 5390 Sears Dower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.2%; Score 36; DB 4; Length 219; 100 0%; Pred. No. 2 8e-06; Live 0; Mismatches 0; Indels
                                                                                                                                                                                         ADDRESSEE: Marshall, G'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                       Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 PGGATGCACTARTAACGGCGGCGAGTGTGGTGGAAT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35 CGGATCCACTACTAACGGCCGCCAGTGTGGTGGAAT 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEFEFENCE/PECET NUMBER: 28113/33072
TELECOMMUNICATION INFORMATION:
                                                                                                                       TITLE OF INVENTION: Receptor Ligand
                                                                                                                                                                                                                                                              STATE. Illinois
COUNTRY: United States of America
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/585,895
                                                                                                                                                                                                                                                                                                                                                                       1BM PC compatible
SYSTEM: PC-DOS/MS-DOS
Sequence 25, Application US/08585895
Patent No. 6245530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/09355700
Patent No. 6361946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38,153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA (genomic)
                                                                         APPLICANT: Alitalo, Kari
APPLICANT: Joukov, Vladimir
                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rest Local Similarity 100 of Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 219 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION POR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CILY, Chicago
STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 60606-6402
                                                                                                                                            NUMBER OF SEQUENCES: 35 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
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                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                    Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
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                                                                                                                                                                                                                                                          STATE.
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                                                                                                                                                                                                                                       CITY:
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TOPOLOGY:
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6300 Sears Tower, 233 South Wacker Drive
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWAPE: Patentin Pelease #1.0, Version #1 25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 28957/34140
                                                                                                                   APPLICATION UNMBER: 08/795,430
FILING DATE: 05-FER-1997
APPLICATION NUMBER: PCT/FF96/00427
FILING DATE: 01-Aug-1996
FILING DATE: 28-JUN-1996
           CURRENT APPLICATION DATA:
APPLICATION NUMBER 35/09/355,750
FILING DATE: 05-NO. 5361946-1999
CLASSIFICATION: Unknown/
                                                                                                                                                                                                                                                                           FILING DATE: 14-FEB-1996
APPLICATION NUMBER: 08,585,895
                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/601,132
                                                                                                                                                                                                                                                                                                                    FILING DAIE: 12-JAN-1996
APPLICATION NUMBER: 08/510,133
                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 01-AUG-1995
APPLICATION NUMBER: 08/340,011
FILING DATE: 14-NOV-1994
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MOLECULE TYPE: chwa

SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-355-700-6
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APPLICANT: Joukov, Vladimir
TITLE OF INVENTION: Receptor Ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 38,153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Illinois
COUNTRY: United States of America
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TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER TRM PC compatible OPERATING SYSTEM PC-DOS/MS-FOS
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, Patent No. 6403088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 219 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Gass, David A.
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INFORMATION FOR SEQ ID NO: 6:
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                                                                                                      PRIOR APPLICATION DATA:
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APPLICANT: Schroeder, Julian I.
APPLICANT: Antosiewicz, Danuel M.
APPLICANT: Clemens, Daniel P.
AFFLICANT: Clemens, Stephan Stephan TITLE OF INVENTION: Nucleic Acids Encoding Metal Uptake IITLE OF INVENTION: Transporters and Their Uses NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATUR: SYSTEM: PC-POS/MS-DOS
SOFTWARE. PALENTIN FELCASC #1.0, Version #1.30
CURRENT AFFLICATION DATA:
APPLICATION NUMBER: US/08/900,148
FILING DATE: 28 JUL-1997
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CGGA1CCACIAGIAACGGCGCGCGGGGGGGGGAAT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.2%; Score 36; DB 4; Lo
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 36; Consorvative 0; Mismatches 0;
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CITY: San Francisco
STATE: California
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NAME: Gass, David A. 38,153
PROTSPATION NUMBER B. 153
EFFER WELL-GARGE LETER WEMBER LETER END TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08966148
Patent No. 5965792
                                                                                        TELEX: 312,,...
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 219 base pairs
"YPE: nucleic acid
"YPE: nucleic acid
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (415) 576-0200
(415) 576-0300
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MEDIUM TYPE: Floppy disk
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LENGTH: 1982 base pairs
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STPANDEDNESS: single
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ZIP: 94111-3834
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; LOCATION: 626..1079
US-08-765-381-1
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                                                                                                                        Gaps
                                                                                                                      0
                                                                               Length 1982;
                                                                                                                0; Indels
OTHER INFORMATION: /product- "low affinity cation OTHER INFORMATION: transporter 1 (LCT1)"
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                                                                           Ouery Match 1.2%; Score 3£; DB 2; Lo
Hest Local Similarity 109.0%; Prod. No. 2.3e-06,
Matches 36; Conservative 0; Mismatches 0;
                                                                                                                                                                               18 CGGATCCACTAGTAACGCCCCCCCCGTGTGTGTGTT
                                                                                                                                                          1 CGGATCCACIAGTAAGGGCCCCCAAGTGTGGTGGAAT 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/AU96/00114
FILING DATE: 05-MAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New York .: UNTIED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/765.381
FILING DATE: 19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN1542/95
FILING DATE: 06-MAR-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER REACABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08765381
Patent No. 6083724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Garden City, New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: PRESSER, LEOPOLD
TELECOMMINICATION INFORMATION-
TELEPHONE: 1-516-742-4343
TELEFAX: 1-516-742-4366
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1079 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: mat_peptide
LOCATION: 191..625
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                                                                                                                                                                                                                                                       RESULT 7
US 08-765-381-1
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                                     US-08 900-148-1
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                                           Caps
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                                                                                                                                                                                                                                                                                   APPLICANT: Christgau, Stephan
APPLICANT: Andersen, Lene N
APPLICANT: Kauppinen, Sakari
APPLICANT: Heldt-Hansen, Hans P
APPLICANT: Dalboege, Henrik
TITLE OF INVENTION: AN ENZYME EXHIBITING MANNANASE ACTIVITY
NUMBER OF SEQUENCES: 15
ADDRESSEE, No. 57957640 No. 5795764disk of No. 5795764th A
  Length 1079;
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                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/525,697 FILING DATE: 21-SEP-1995 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
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                     6.69-06;
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Pred. No. 6.5e-06;
                                                                                                       1 GSATOCACTAGIANACOSCOSOCACIAGIGSIGGAAT 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.1%; Score 35; DB 3;
100.0%; Pred. No. 6.6e-0
tive 0, Mismatches
                                                                                  2 GGATCCACTAGTAACGGCCGCCAGTGTGGGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        405 Lexington Avenue, 64th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.1%, Score 35, DB Best Local Similarity 100.0%; Pred. No. 6.55 Matches 35; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: United States of America ZIP: 10174-6401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCMFUTER: IBM FC compatible OPERATING SYSTEM: PC-TAGS/MS-FOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: DK 0485/93
FILING DATE: 30-APR-1993
                                                                                                                                                                                                                            ; Sequence 1, Application US/08525697
• Patent No. 5795764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38,711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEFERENCE/INDCKET NUMBER:
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                   Best Local Similarity 100.(
Matches 35, Conservative
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EDNESS: single
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                                                                                                                                                                                                           US-08-525-697-1
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  Query Match
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RESULT 11
Us.08-454-557C-75/C
Us.08-454-557C-75/C
Sequence 75, Application US/08454557C
Fatent No. 5830670
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wands, Jack R.
TILLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TILLE OF INVENTION: 11-11 Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 75, Application US/UR34U426D
Patent No. 5948634
GENERAL INPORMATION:
APPLICANT: dc la Monte, Suzanne
APPLICANT: dc la Monte, Suzanne
APPLICANT: Monds, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEPTEMPERS: 121
COPPESSONDENCE ALORESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.9%; Score 29; DB 2; Length 115;
100.0%; Pred. No. 0.003;
ive 0; Mismatches 0; Indels
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1100 New York Avenue, Suite boo
                                                                                                                                                                                                                                                                                                                                         : Sterne, Kessler, Goldstein & Fox P.L.L.C.
1100 New York Avenue, Sutte 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARF: PatentIn Release #1 0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,557C
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Best Local Similarity 100.0%; Pred. No. 0.0
Matches 29; Conservative 0; Mismatches
                            5.0 CSGATOCACIA/STAA/OSCOGCCAGI/GI/GE 79
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30-MAY-1995
N. F.:
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IELECOMMUNICALION INFORMATION:
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ. ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALTOKNEY AGENI INFORMATION:
NAME: Ludwig, Steven R.
PEGISTPATION NUMBEP: 36,203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: ZUUU5-3934
COMPUTER READARLF FORM:
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: both
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US-08-454-557C-75
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                                                                                                                        TITLE OF INVENTION: MONOCLONAL ANTIBOIDES THAT RECOGNIZE ANTIGENS TITLE OF INVENTION: ASSOCIATED WITH TUMOR METASTASIS TITLE OF INVENTION: ASSOCIATED WITH TUMOR METASTASIS CURRENT FILL REFERENCE: SUNY CURRENT FILLNG DATE: 1999-06-15 NUMBER OF SEQ ID NOS: 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                    1.1%, Score 33, DB 4, Length 870, 100 0%; Pred No 4 90-05;
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655 15th St., NW, Suite 330 - G Street Lobby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MUNROF, Donald G
APPLICANT: VYAS, Tejal B.
TITLE OF INVENTION. A HUMAN EDS-6 PECTEPTOR HOMOLOW:
NUMBER OF SEGUENES: 7
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COMPUTER: Floppy disk
COMPUTER: TEM PT. COMPTER: COMPUTER: COMPUTER: PATCHIN: COMPUTER: Patchin Pelease #1.0, Version #1.30
CURRENT APPLICATION DATA:
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Matches 33; Conservative 0; Mismatches
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... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-MAY-1997
Sequence 1, Application US/09333599
Patent No. 6245898
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, Patent No. 6020158
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                                                             APPLICANT: Testa, Jacqueline E. APPLICANT: Quigley, James P. APPLICANT: Seandel, Marco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (202) 638-5000
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TYPE: nucleic acid
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Matches 30, Conservative
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
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                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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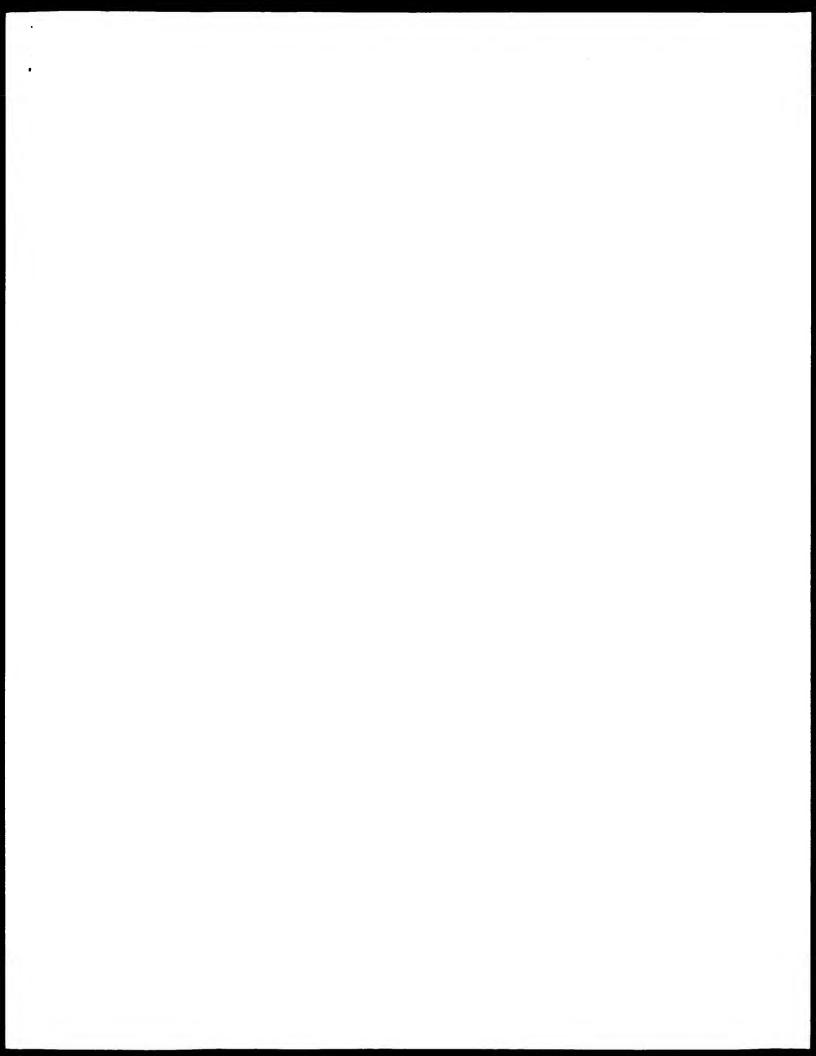
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Gaps

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APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
FITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
FITLE OF INVENTION: of Alzheimer's Disease
CORRESPONDENCE: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.98; Score 29; DB 2; Length 115; Best Local Similarity 100 6*: Pred No. 0.004; Matches 29; Conservative 0. Mismatches 0, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Sterne, Kessler, Goldstein & Fox P.L.L.C.
1100 New York Avenue, Suite 600
                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE. Fatentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36, 203
REFERENCE/DOCKET NUMBER: 0609.3840004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371 2600
TELLEPAX: (202) 371 2540
                                                                                                                                                                                                                                                     0609.3840002
                                                                                                               US/08/340,426D
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FILING DATE: 30 MAY-1995
CLASSIFICATION: 530
MEDIUM TYPE: Floppy disk
COMPUTER: IHM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPFRATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5948888
                                                                                                                                                                                                                                              REFERENCE/TOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 75.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                               36,203
                                                                                                                                   FILING DATE: 14-NOV-1994
                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                          NAME: Ludwig, Steven R. REGISTRATION NUMBER: 36
                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 115 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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TYPE: nucleic acid
STRANDEDNESS: both
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                                                                                                               APPLICATION NUMBER:
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US-08-340-426D-75
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APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and
TITLE OF INVENTION: Detection of Alzheimer's Disease
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.99; Score 29; PB 5; Longth 115;
LOULUK; Pred. No. 0.004;
LVE 0; Mismatches 0; Indels
  0.9%; Score 20; DB 2; Length 115;
100.0%; Pred. No. 0.003;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Sterne, Ressler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE Patentin Parease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER PST,0895,12111A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Boursnell, Michael E.G.
APPLICANT: Inqlis, Stephen C.
TITLE OF INVENTION: Viral Preparations, Vectors,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Viral Preparations, Vector TITLE OF INVENTION: Immunogens, and Vaccines CORPHESE OF SEQUENCES: 25
CORPHESE NUMBER OF SEQUENCES: 25
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                                                                                                                                   1 CGGATCCACTAGTAACGGCCGCCAGTGTG 29
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                                                                                                                 RESULT 14
PCT-US95-17111A-75/C
Sequence 75, Application PC/TUS9517111A
GENERAL INFORMATION:
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FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
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, Patent No. 6287557
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PEGISTRATION NIMBERS: 45,203
FFFFERN'E, Impress: 100 TELECOMMUNICATION:
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INFORMATION FOR SEQ 1D NO: SEQUENCE CHARACTERISTICS:
Query Match
Best Local Similarity 100.0
Matches 29; Conservative
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TYPE: nucleic acid
STRANDEDNESS: both
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Bost Local Similarity Tould
Matches 29; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington
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ZIP: 20005-3934
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PCT-US95-17111A-75
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STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
COUNTER: USA
COUNTER: USA
COUNTER: USA
COUNTER EADABLE FORM:
MEDIUM TYPE: PIOPPY disk
COMPUTER EADABLE FORM:
MEDIUM TYPE: PIOPPY disk
COMPUTER EADABLE FORM:
MEDIUM TYPE: PIOPPY disk
COMPUTER EADABLE FORM:
COMPUTER EADABLE FORM:
MEDIUM TYPE: PIOPPY disk
COMPUTER EADABLE FORM:
MEDIUM TORM:
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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(without alignments)
11504.298 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No is the number of results predicted by chance to have a

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

RESULT 1 GGA271386	
LOCUS	GGA271386 3111 bp mkNA linear VRT 23-MAY-2001
DEFINITION	•
	gene).
ACCESSION	AJ271386
VERSION	AJ271386.1 GI:7799040
KEYWOPDS	bodo gene; beta-carotene 15,15/-dioxydenase.
SOURCE	chicken.
ORGANISM	Gallus gallus
	Fukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
	Phasianinae; Gallus.
REFERENCE	1 (bases 1 to 3111)
Ail Heres	Wyss.A., Wirte, G., Weggen.W., Brugger.F. Wyss.M., Eriedlein, A.,

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Best Local :
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21134366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (18-JAN-2000) Wyss A., Vitamins and Fine Chemical Division, VFHC, F. Hoffmann-La Roche Ltd., Building 93/814, CH-4070
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Cloning and expression of beta,beta-carotene 15,15'-dioxygenase
Bioshem, Biophys. Res. Commun 271 (2), 334-336 (2000)
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                                                                                            CACAGGAGAGGGATGGAGACAATATTTAACAGAAACAAAGAAGAAGAAGCATCCAGAGCCCATA
                                                                                                                              AGCTGTTCTTAGCCCAGAGAGAGGAGGGCACCGTACGCCTGCAGCAGCTGGGTAGAGGA 120
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                   AAAGCTGAGGTGCAAGGTGAGTTGCCCACTTGGTTGCAAGGGGTACTTCTCCGAAAATGGC
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/country="Switzerland"
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KNIFAKAFSYLSHTIPEFTDNCLINIMKTGDDYYATSETNFIRKIDPQTLETLDKVDY
KNYAVNLATSHPHYDSAGNILMMGTSIVDKGRTKYVLFKIPSSVPEKEKKKSOFKHL
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/product="beta-carotene 15,15'-dioxygenase"
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/translation="METIFNRNKEEHPEPIKAEVQGQLPTWLQGVLLRNGPGMHTIGD
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/db_xref="GI:7799041"
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/EC_number="1.13.11.21"
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Beta-carotene 15.15 dioxygenase
Furant EF 1031627-A 2 To Aug. 2000;
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HEINMICH RACCHIMAN, POLAND BURUGERH, ARNO MARTIN FRIEDLAIN, PI
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Qy Db	Query Best Match	BASE COUNT				Sou	TITLE JOURNAL FEATURES	REFERENCE AUTHORS	KEYWORDS SOURCE ORGANISM	LOCHS DEFINITION ACCESSION VERSION	RESULT 4 AX400072	Qу	Оy	Qy Db	Фу	Qу	מא מא	Ωţ
128 GAGGGATGGAGACAATATTTAACAGAAACAAAGAAGAGAGACCAGATCCAGAGGCCCGATAAAAGCTG 187 	Query Match 25.8%; Score A94; DR 5. Length 2286, Best Local Similarity 70.0%; Pred No. 4 Le-164; Matches 1112; Conservative 9, Mismatches 470; Indels 6; Gaps 2,	en.	TEVFCSIPSRSLLSPSYYHSPGVTENYVIFLEOPPFLDII.KMATAYTPPMSWAS;T.AF HREEKTYIHIIDORTBOPVOTKFYTDAMVYEHYVNAYEEDOGIVFDVIAYEDNSIYOL FYLANLNODEKENSRLTSVOTLRFRFAVDIHVTAVKANAVETORATAI.KEEDS; VYCOPDETLYBGLELPPNYYAHNGKOYRYYDATGVWGSPIPTKIIKYDIITXSSHXREE	<pre>/translation="MDIIFGRNRKEQLEPVFAKVTGKIPAMIQGTLLFNGFGMHTVGF SRYNHWFDGLALLHSTIFNGFVYF9SKYLBEDIYMTNIEANEIVVBEKKOGKSPWHTVGF KNIFSKAFSYLSHTIFDFIDNCLINHMGGEDFYATSFTNYIRKINPQTLETLEKUDY RKYVAVNLATSHPHYDEAGNVLNMGTSIVEKGKTKYVIFKIPATVPEGKKOGKSPWKH</pre>		rce	Nucleic acids and polypeptides L Patent: WO 0218424-A 243 07-MAR-2002; HYSEO, INC (TS) Location/Qualifiers		human. Homo sapiens Eukaryota; Mcta	2286 bp DNA linear FAT 96-JUN-2002 TION Sequence 243 from Patent WOO218424. CON AX400072 AX400072.1 GI:21336495		3061 CCATAAAATGGAAATAAACACCTCCATAATAAAAAAAAAA	3001 CACTGGGGTCAGATCTAGAGCTTAAGTAAGCAGTCTGGGGTTTTCAAATGTTTATAATGTT 3060	2941 TGCTGTCTTTATGGTTTGCATGTATGAAGAATACACTGCCTAATTCTAATGTTAAAAAGT 3000	2881 CAGAGCAGCAATAGAACCAACACCATCCACAGFFCFFTGCTFTGCT	2821 CATCACATAAGAACAATGGGGCTTTGGTGACTTGTTCATGATTACATAAGATGTTTGCAG 2880	2/61 CTACTCACTGTATTTTGCAGGACAGAACAGAAATGACACTGTCACTGTACGCCC 2820	2701 ATGTGACACCACGCIGITIGGGTATCTCICACTTTCACATACCTGTTCTCATGGTTTCTG 2760
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Submitted (16-FBB-2000) Takao Isogai, Helix Research Institute,
Genumics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:qenomics@hri.co.)p, Tel-81-448-52-375, Fax.81-438-52-3786)
NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan: cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology Center
otto.) and Department of Virology, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H., Wagatsuma,M., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K., Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AK001592 1 GT-7022940 oliqo capping; fis (tull insert sequence). Homo sapiens teratocarcinoma cell_line:NT2 cDNA to mKNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A.,
Nakamura,Y., Nagahari,K., Masuho,Y., Ninomiya,K. and Iwayanagi,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AK001592 apiens cDNA FLJ10730 fis, clone NT2RP3001307
                                                                                                                                                                                                                                                                                                                                                                                                                                    Isoqai, T. and Otsuki, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEDO human cDNA sequencing project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isoqai, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Primates; Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone_lib:NT2RP3 clone:NT2RP3001307.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases ! to 2427)
                              /organism-"Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                Location/Qualitiers
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                                                      TTAAGATCCCTGCCACAGTACCAGAGGGCAAGAAGCAGGGGAAGAGCCCCTGGAAGCACA
                                                                                                        GTGAGACTAACTTCATCAGAAAAATTGATCCACAGAGACTCTGGAGAGACACTAGATAAGATAAG
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/cell_type-"toratocarcinoma"
/clone_lib "W12FP3"
/note="cloning vector: pME18SEL3-mRNA from WT2 neuronal
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                                                                                                                                                                                                                                                              Homo sapiens beta,
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600 N. Wolfe Street, Baltimore, MD 21287, USA
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Cloning and characterization of a human beta, beta-carotene 15,157
dioxygenase that is highly expressed in the retinal pigment
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 2446)
                                                                                                                                                                                                                                                                                                               TGCACACAATAGGGGACACTAAATAGAACCACTGGTTTGATGGCTTGGCTCTGCTGCACACG 307
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MHMDLHGLF1TDMDWDTKKQAASEFQKDRASDCHGAPLT"
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#YLANLN@DFKENSKLISVFTLRKFAV/LHVLKNAEVGINLIKVASTTATALKEEDGQ
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TEVFCSIPSRSLISDSYYHSEGVTENYVIFLEQPFRLDILKMATAYIPKMSWASCLAF
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/[translat.on-*MollifGRNRKEQLEPVPAKVTGKIPAWLQGTLLENGPGMHTVGE
SEYNHWEDGLALLHSETIFDGEVYVPSKYLESDTYNTNIFANRIVVSSEGTMAYPDDC
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3 (bases 1 to 2117)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (22 MAY 2009) Wyse A., Vitamits and Fine Chemical Division, VFHC, F. Hoftmann-La Roche Ltd., Building 93/814,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wyss, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Expression pattern and localization of beta, beta-carotene 15,15'-dioxygenase in different tissues Biochem, J. 354 (Pt 3), 521-529 (2001)
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Wyss,A., Wirtz,G.M., Weggen,W.D., Brugger,R., Wyss,M.,
Friedlein,A., Riss,G., Bachmann,H. and Hunziker,W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus
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/moduct="beta_beta-gareteme_15,15'-dloxygemase"
/mrotein_id="0AB92531.2"
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/clone_lib-"Sugare mouse kidney mkia"
/dev_stage="adult"
AEVECSISSESELSPSYYHSEGVTENYVVFI EQPEKIDII-KMATAYMRGVSWASC
                                                                                                                                                                                                                                                                                                                                                                        /gene="bCDO"
/EC_number="1.13.11.21"
/function="centric cleavage of beta carotone"
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179. .1879
                                                                                                                                                                                                                             /protein_id="CAB92531;;
/db_xref="GI:11990268"
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YYCQPEVLYBGLELPPTUAYNKFYPHYIFAAEVCMSBVPTKTLKYDITIKSSLKWSE
ESCWPAEPLFVPTVGAKDEDDGVILSAIVSTDFQKLPFLLILDAKSFTELARASVDAD
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                                                                                                                                                                                                 Yan,W., Jang,G.-F., Haeseleer,F., Esumi,N., Chang,J., Kerriqan,M. Campochiaro,M., Campochiaro,P., Palczewski,K. and Zack,D.J. Cloning and characterization of a human beta, beta carotene
Submitted (09-AUG-2000) Ophthalmology, Johns Hopkins University,
                          Direct Submission
                                               Yan, W., Jang, G. F., Haeseleer, F., Esumi.N. Or
Campochiaro, M., Campochiaro, P., Palczewski, K.
                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                       Eukaryota, Metazma, Chordata, Craniata, Vertebrata, Enteleostomi;
Mammalia; Eutheria; kodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 2119)
                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AFF94888 (Bodo) mRNA (1900) MCO) mRNA, (1900) MCO) mRNA, Mus musculus beta, beta-carotene (5,15'-dioxygenase (Bodo) mRNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGCCCATCTTTGTTCCCAGCCCCGATGCAAGAGAAGAAGGATGAAGGTGTTGTTTTGACC 1554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAACTGAATGTGCAAACAAAGGAAGTACTGCACTGGGGAAGAAGAACCACTGCTGGCCCTCA 1494
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Tang,G -F , Haeseleer,F
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                                                      and
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                                           648 AAGGITGATTACCGGAAGTATGTGGGGGGAAAACCTGGGTAACCTCGCACCCTCAITATGAC
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AGTGCTGGAAATATTCTCAACATGGGTACTTCAATTGTTGATAAAGGGAGAACAAATAT 720
                                                                                           AAGGTAGACTACAGCAAATATGTAGCTGTAAACTTGGCAACTTCTCACCCACACTATGAC 660
                                                                                                                                                                                                                                                                           ATTCCTGAGTTCACGGACAACTGCCTGATCAACATTATGAAAACTGGGGGATGATTATTAT
                                                                                                                                  GCAACCACGGAGACGAACTACATUAGGAAAATUGAUUUUCAGAUUUTAGAGACCTTGGAG
                                                                                                                                                                                                                                ATCCCCGACTTCACAGACAACTGTCTGATCAACATCATGAAATGTGGAGAAGACTTCTAT
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/product="beta, beta-carotene 15,15'-dioxygenase"
/protein_id="AAG15381.1"
/db_xref="Gi:10242318"
/translation="MEIIFGQNKKEQLEPVQAKVTGSIPAWLQGTLLRNGPGMHTVGE
SKYNHWFDGLALLHSFSIRDGEVFYRSKYLQSOTYIANIEARITVSEEGTMAXPDPC
KNIFSRAFSYLGHTIPDFTDNCLINIKNGGEDPYATTETNYIAKIEDGTLETLEKVUP
KRYVAVNLATSHPHYDEAGNVLNMGTSVVDKGRTKYVIFKIPATVPDSKKKGKSPVKH
AEVFCSISSRSLLSPSYTHSFGYTENFYLDHVVFHHVNAXEEDGCYLFDVIAYEDSSLYQL
FYLANIKNDFEKKSRLTSVPTLKRFANPLHVDKDAEVGSSLYKVSSTTATALKEKDGH
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ESCWPAEPLFVPTPGAKDEDDGVILSAIVSTDPQKLPFLLILDAKSFTELARASVDAD
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/tissue_type-"kidney"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="Bcdo"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1008 GACAGGGAGACAAGACATACATTCATCATCGACCAGAGGACCAGGAAGCCTGTGCCT 1067
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                                                                                                                                                                                  TTCAAAGAATTGGGCCGAGCCACAGTTAACGTAGAAATGCATCTGGACCTGCATGGGATG 1674
                                                                   TTTATCCCAGATGCAGACTGGAATGCAGTGAAGCA 1752
                                                                                                                                                                                                                                                     GCCATCGTCTCTA(156A)C1CCAAAA6CTGCCTTTTTA(ACTCATTCTGGATGCCAAAAGT
                                                                                                                                                                                                                                                                                              TGTGTTGTGGTGTCTGAGCCAAATAAAGCACCCTTCCTACTCATCTTGGAIGCIAAAACA 1614
                                                                                                                                                                                                                                                                                                                                                                                     AAACTGAATGTCCAAACAAAGAAAGTACTESCACTSSSATAGAAGACCACTSCTGGCCCTSA 1494
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                                                                                                                                                          TTTACGAAACTGGCTCGCGCTCTTTTTTTGATGCGACATGCACCTGGACCTCCATGGTTTA 1727
                                                                                                                                                                                                                                                                                                                                            GAGCCTCTGTTTGTTCCCACGCCAGGTGAGGTGAAGGATGAAGATGAAGTCATTTTATCA 1607
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Q	Query Mat Best Lock Matches Qy Db	CDS BASE COUNT	VERSTON KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE JOHPNAL FEATURES SOURCE	AF271298 LOCUS DEFINITION ACCESSION
241 CCAGGGATGCACACATAGGGGAACATAAALACAACCACTGGTTGGTTGGTTGATGCTCACACCAGGCAACATGCACTTGCACACACCAGGCAACCATTGCTCACACACCATTGCTTGATTGCTTGACACCACCAGGCAACAACAACCATTGCTTGGTTGATTGCTTGAACACCATTGCTTGACACCATTGCTTGACACCAGGCAACCATTGCTTGACACCAGACCTTGCTTG	7 (0)	Adb_xref="taxon:10090"	it-	AF271298 2137 bp mRNA linear ROD 27 FEB 2001 Mus museulus beta-carotene 15,157-dioxygenase mRNA, complete cds. AF271298
Db Qy Db	Q B Q F Q	3 4 7 4 8 4 8 4 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	\$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$	ф
	1138 TPAAAAAANTGGACAAAGACHCTTPGAAGGCAACACAACAACAACT FACGTCCCAACCTGC 1197 1266 CTPACAACACTGC 1111 111		541 GETAGE ASTECACASA AACTESTSTATE AAAANT GATEATAAATSTEGAAAAAAAAAAAAAAAAAAAAAAAAAA	486 GOCTAGOCGGAGOGGGAAAAAAAAAAAAAAAAATTIIGTCCTAGTTGTCTCACACC 545 481 AUDOCUGAGTDCACGGACAAA DGCCDGAUCAAAAAAATTIIGTCCTAGTTGTCTCACACC 540

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                                     180 AAAAGCTGAGGTGAAGGTCAGTTGCCCACTTGCAAGGGGGAACTTCTCCGAAATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (08-JUN-2001) Kimiraka Takitani. Osaka Medical College, Department of Pediatrics; 2-7 Daigakumachi, Fakatsuki, Usaka 569-8886, Japan (E-mailped016@poh.osaka-med.ac.jp, Tel:81-726-83 1221(ex.2476), Fax.811-726-84-6554)
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SEVFCSIPSRSLLSPSYYHSFGVTENYVVFLEQPFKLDILKMATAYMRGVSWASCMTF
CKEDKTYIHIIDQKTRKPVPTKFYTDPMVVFHHVNAYEEDGCVLFDVIAYEDNSLYQL
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/product="beta-carotene 15,15'.-dioxygenase"
/protein_id="BaB60807.1"
/protein_id="BaB60807.1"
/db_xref="GI:14349294"
/translation-"MEIIFGRNKKEQLEPLRATVTGSIPAWLQGTLLRNGPGMHTVGD/
/translation-"MEIIFGRNKKEQLEPLRATVTGSIPAWLQGTLLRNGPGMHTVGD/
KYNHWFDGLALLHSFSIRPGEVFYPSKYLQSTTYNGANIEANELVUVSEFGTMAYPDDPC
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ESCWPAEPLFVPTPGAKDEDDGVILSALISTDPQKLPFLLILDAKSFTELARASVDVD
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                                                             CAAACTTCCA---ACTTCCGCAACIGCIGIIGIAAAAGAAAAAGAIGGCAGCATCTATTCTCA 1414
                                                                                                                                                                                            CCTGGCCAACATAAAAAAACTTCAAGAAAAATCCAGGCTGACCCCACGCCCACCCCT 1453
                                                                                                                                                                                                                                                                                            CGGCTGTGTGTGTTTGATGTCATCGCCTATFAAFACAACAGTCTCTATCAGCTCTTCTA 1393
                                                                                                                                                                                                                                                                                                                                                                                   AACCAAATTCTACACAGAGGCCATGGTGGTCTTCCACGAFGTTAATGCCTATGAGGAGGA
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                                                                                                                                                      <u> Ο ΑΑΘΕΘΟΤΤΤΑΊ ΤΙΣΕΙΣΟ ΤΙ ΕΙΣΟΝΙΑΙ ΚΑΙ ΤΑΤΑΙΑΝΑΙ ΕΙΣΑΙΑΝΙ ΕΙΣΑΙΑΝΙ ΤΑΙΣΕΙΤΑΙΤΈ ΤΑΙΘΕΈ 12%</u>
                                                                                                                                                                                                                                               CTTAAAAAAAACTGGACAAAGACTTTGAAGTGAACAACAAGCTTACCTCTATCCCAACCTG 1196
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Oy 132 GATGGAGACAATATTTGAACAGAAACAAAGAAGAAGGATCCAAGAGCCCATAAAAAGCTGAGGT 191	Query Match 18.6%; Score 577.2; DB 6; Length 1773; Best Local Similarity 6) H*; Pred No / 20-115; Matches 972; Conservative 0; Mismatches 588; Indels 12; Gaps 3;	EPVFIPRPGAVDEDDGVVLTVIINNKPLUGGFLLVLDAKSFKEIAFACLDVEIHMDMH GYFIPGSS" BASF COUNT 556 4 360 C 405 g 451 t	VCTLPCKSLLTPSYYHSFGMTDNYFIFIEOPLKLDILKMATAYLRFVSWASCMKFHPE DSTLTHLDRNTKKEVATKFTDAMTVYHOVNAFEDDGHVVEDVILAYDDNNLXEFFYL NKLKETMGATNLYCKFKFTKFVEPLSDVG-EFFSEDLVKLKYFTASAVKFKIBJK INCOBE VLCEGVELDRINYKFNGKKYRYSYMCCVDESPVAKTKYKLKYTAKTONJEMKGDDJEAS VLCEGVELDRINYKFNGKKYRYSYMCCVDESPVAKTKYKLKYTATAYTKOJTFKOJTFKOJTFKOJTFKOJTFKOJTFKOJTFKOJT	/translation="MQYDYGKNKRFFHPEPIKTEVKGSIPFWV@GTLIENGF@MESVGF TTYNHWEDDMALLHSFAINKGFWTYRSRYLRGDTYNSNMQANRIVVSEMGTMAYPDPC KNIFSKVITFELSHTIPDEFIDNGGNNILKYGNDFHATSEINVIKIDEVTLETQEKIDV LKYLDVSIVASHTHYDKEGNSYSMGTCIAEKGKTNYMLEKVPGGSRPDGSRPLKSAEA	/note="unnamed protein product" /codon_start=1 /protein_id="cAc5q782.1" /dh_xref="q1.15143070"	rce	JOURNAL Patent: Wo 0148167-A 16 05-401-2001; Greenovation Filanzenbiotechnologie GmbH (DE) FEATURES Location/Qualifiers	ACtinopheryqii; Nacpterygii: Telogstel; Ustariophysi; Cypriniformes; Cyprinidae; Danio. REFERFNOE 1 (bases 1 to 1773) AUTHORS von Lintig, J. and Vogt, K.	Ï	DEFINITION Sequence 16 from Patent WOO148162. ACCESSION AX189590 VERSION AX189690.1 GI:15143069	PESULT 11	Qy 1674 GTTTATACCACAGAATGATTTGGGGGCTGAGACGGA 1709	Qy 1614 ATTCAAAGAATTGGCCGAGCCACAGTTAACGTAGAAATGCATCTGGACCTGCATGGGAT 1673	Qy 1554 CTGTGTTGTGTGTCTCTGAGGCAAATAAAGGAGCAGCTGTGGATGTTGGATGTTAAAAG 1613	QY 1494 AGAGGTATATTATATATATATATATATATATATATATAT	QY 1434 AAAACIGAALGICCAAACAAAGGAAGTACIGCACIGGAGGAGAACACCACIGCTGGCCCCC 1493	QY 1374 AAAATACAAGTATGTCTATGCAACAGAAGTCCAGTGGAGGCCCAGTTCCTACAAAGATTGC 1433 	
	1152 CAAARACEERAAARACAARACAARACEERACEERAAACEERAAGCEERTEEREEREEREEREEREEREEREEREEREEREEREER		1032 TGATGCTFTGGTGCTTTATCACCACATAAATGCFTACGAAGAAGATGGCCACGTTGTTFT 1091	972 - GAPATRONI FRANKETESIASAPASAAAAAAAAAAAAAAAA AARI ATGCACCAAGI ETI ACAC 1031 	912 AACHSOCIACATCCGASTISTEAACIOSSTI CCHACHTECCHI CATAACGAGGATAA 971 	52 CACAGAAAATTATATTGTGTTCATAGAGCAGCCATTTAAACTGGATATTGTCAAACTGGC 	742 ASTATOS DE ADECEMBRACIONES DE LA ARCHAMA DE LA CAMBRILLO DEL CAMBRILLO DE LA CAMBRILLO DE	32 SATEMETER (1951) ISTAN ASAAAAAAAAAAAAAAA TETETETAAA TAYAAATEE 11 JUUR 15 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	772 TRITUTICACA POGGIACITICAN IGLIGATA MAGGIAGACAMA ATATOLICICI HAN 	12 CAGCAAATATGTGTAAACTTGGGAAACTTGCACGACACTAGGAGAGTGGTGGAAAA	552 GACTAR TECATICAGAAAAATTGATO AYAGA TOTGGAGA AYTAGATAAGATAGA TAGATAGATAGA TAGATAGATAGA TAGATAGA	72 M. SANTER AND THE TERMEN AND A LABORATED TO SANTER THE TOTAL AND THE SANTER AN		372 CTSCARIA HABANS ANACCSARICS ESSISTIMAN 1 1 1 1 1 1 1 1 1	12 CACGTTTAAAATISSTGAASTTTACTACASAAGIAAGIACGTACCTCCCAAGTTACACACATACACACATACACACATACACACATACACACATACACACATACACACATACACACATACACACATACACACATACACACATACACACATACACACATACACACATACACACATACACACATACACACATAC	SZ CARAPASSSACACTAATAKAACCACTSSTITAATSACTISGETEGGEGEGAKAKETT 13 CECTGEGAAMAANAMATATATATTITTITTITTITTITTITTITTITTITTITTI		

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Direct Submission
Orect Submission
Orect Submission
Submitted (25-JAN-2001) von Lintig J.,
Submitted (25-JAN-2001) von Lintig J.,
                                                                                                                                                                                                                           Universitaet Freiburg, Hauptstrasse Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                        Identification and Characterization of a Mammalian Enzyme Catalyzing the Asymmetric Oxidative Cleavage of Provitamin Biol. Chem. 276 (17), 14110-14116 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Danio rerio
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1 (bases 1 to 1774)
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Actinopterygii; Neopterygii, Teleostei,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               b,b-carotene-15,15'-dioxygenase; b-diox gene
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/product="putative b,b-carotene-15,15'-dioxygenase"
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                                                                                                                                                /tissue_type="liver"
                                                                                                                                                                                         /organism="Danio rerio"
                                                      /gene="b-diox"
                                                                                           /gene="b-diox"
                                                                                                                               /dev_stage-"adult"
                                                                                                                                                                        /db_xref="taxon.7955"
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                                                                         Eukiryola; Metazoi, Chordata, Craniata; Vertebrata, Euteleostomi, Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo l (bases 1 to 2051)

Au-Young, J. Bandman, G., Tang, Y.T., Yue H. Azimzai, Y., Burferd, N. Bandman, M.R., Lu, D.A., Hillman, J.L. Patterson, C. and Lal, P.
                                                                                                                                                                                                                                                              Sequence 24 from Patent W00107612
AXU78356
AXU78356 1 GI:13158025
                    Receptors and associated proteins Patent: WO 0107612-A 24 01-FEB-2001; Incyte Genomics, Inc. (US)
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                                                                AAACGCACTGGACAGCTCCITCCAGGGAGATACTACAGCAAACCTTTTGTTACATTTCAT 1165
                                                                                                       AGAAAGACGAAAAAAAGAAGTATCCACCAAGTTTTACACTGATCCTTTGGTGCTTTATCAC 105
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Submitted (08-JUN-2008) Cell Biology and Melecular Genetics,
University of Maryland, Microbiology Building, Campus Drive,
College Park, MD 20742, USA
                                                                                                                                                               Cunningham, F.X.
                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens putative carotene dioxygenase mRNA, complete cds. 
 {\rm AF276432}
                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                  An ortholog of the human retinal pigment epithelium protein RPE65
                                                                                                                                                                                                                                        Cunningham, F.X.
                                                                                                                                                                                                                                                      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2597)
                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata, Euteleostomi;
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                                                                                                                                                                              (bases 1 to 2597)
/db_xref="taxon.9606"
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Match 8.9%;
Local Similarity 51.4%;
1386 AAGGIGGACCIIGGGGAGAAACCAIGGAGGCCAGGTGATATGTTCTATTGCTTCTACA 144
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                                                                          754 ANAGANAAGAAGAAATCTTGTTTTNANCACCTGGAAGTAGGTATGCTCCATCCCCTTCTCGC 813
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GFFHLVGISLTKVIVVNKTTWGSHENLHQEDLEKEGGTEFIQTYYDRESGKKYHFFYGG
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KNKIVISEFGTLALPDD;KNVFEKFMSKFELPGKAAAMIDNINVNYVKYKGDYYLCTE
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/protein_id="AAK69433.1"
/db_xret="GI:]458226"
/translation="MGNTPQKKAVFQQCPGLPGVAPITTVEFAPROISAKVWGHFPK
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RPE65; putative carotene eleavage enzyme"
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/hote-"7 pooled tumors
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Pred. No. 9.1e-50;
0; Mismatches 708;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1381 AAGTATGTCTATGCAACAGAAGTCCAGTGGAGCCCAGTTCCTACAAAGATTGCAAAACTG 1440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1282 GTAAAAGAAAAAGATGGCAGCATCTATTGTCAACCTGAAATATTATGT------ 1329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1225 GACAAGGATGCAGAAGTAGGTTCTAAFFTAGTGAAAGTTCC - AAGTFCCGCAAGTGCT 1281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1054 CACATAAATGCTTACGAAGAAGATGGCCACGTTGTTTTTGATAT------CGTTGCC 1104
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                                                                               AK027801 1983 bp mRNA linear PRI 01-AUG-200 Homo sapiens cDNA FLJ14895 fis, clone PLACKHUU4646, weakly similar to B.taurus mRNA for retinal pigment epithelial membrane receptor
                                AK027801
                                                                                                                                                                                                                                                                                      CC
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400 GEGETELGAGITTIGGAACCALGGCHAECCGGATCCALGCAAAAACATATTIG------CC 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                    150 GAARAGEATOCARRAGOCCATAAAARCEGAGGEROAAGEGEGAGTEGACCTEGGTEGOCAA 219
                                                                                                                                                                                                                                                                                                          220 GGGGGATATTCTCCGAAAATAGGCCCAGGAGGGAGAATAAAATAGGGAGAGATAAAATAGAC 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@fricoip, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'-& 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oliyo capping; lis (tuli insert sequence).
Homo sapiens placenta cDNA to mRNA, clone_lib:PLACE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                University of Tokyo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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Matsunawa,H., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J.,
Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y. and Sasaki,N.
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                                                                                                            AGAAGTAAGTACCTCCGAAGTGACACACACAACTGCAATATAGAAGCAAAGCAAACCGAATCGAA
                                                                                                                                                                                                                           TGSTTTGAPGGCTTGGCTGCTGCACAGCT::CACGTTTAAAAAIGGTGAAGTTTACTAC 339
                                                                                                                                                                                                                                                                                                                                                                                               GAAGAGGCTCCACGGGGCATCTCTGCTCGAGTCTTGGGGACATTTTCCTAAGTGGCTCAAT 243
                                                          AGGAGCAAGTTTCTACAGAGTGATACATA1AAGGCCAACAGTGCTAAAAAACCGAATTGTG 423
                                                                                                                                                                       TGGTTTGATGGGATGGCGCTGCTTCACCAGTTCAGAATGGCAAAAGGGCACAGTGACATAC
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KNRIVISEPGTLALPDCKNVFEPFMSPFPI.PGKAAAMTDNTNVNYVFYKGDYYLCTE
TNEMNKVFLETLEKTFKVFWSKFIAVNGA.FAHPHYFPEGTAYNMENSFGPYGFSYKVI
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LSELSYTSASAVKQAF«TI WYSHENILJEELLEK ÞÍÐGTEFÞQTYYDRESGKKYHFEYGO
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TSK I PGKAFSIKTI SWEPQMNT REHVVEK ETGQI I. DGFYYSK PEVT FHQTNAFET©GCV
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/clone_lib="PLACEI"
/note="cloning vector: pME18SFL3"
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ALIGNMENTS

Source	FEATURES				COMMENT	JOURNAL		TITLE	SHOHLIN	REFERENCE				ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION			NOTEINIABE	POCHS	RESULT 1 BI389779	
1661 /organism="Gallus gallus"	Email: orgonnender.equ, www enlokest nder.equ.	Fax. 302-831-2822	Tel: 302-831-1335	University of Delaware	Contact: Larry A. Cogburn	Unpublished (2001)	library USDA/IFAFS Animal Genome Project	ESTs from Primary Chicken Pituitary/Hypothalamus/Pineal cDNA	Porter, T.E. and Cogburn, L.A.	1 (bases ! to 661)	Phasianinae; Gallus.	Archosauria; Aves; Neognathae; Galliformes; Phasianidae;	Eukaryota, Metadoa, Chordata; Craniata; Vertebrata; Euteleostomi;	Gallus gallus	chieken.	EST.	BI389779 1 GI-15083061	BI389779	dallus] mRNA seguence	Library Gallus gallus cDNA clone pgplc.pk002.a13 5' similar to	pgplo pk802.al3 Primary Obicken Fituitary/Hypothalamus/Pincal	BI389779 661 bp mPNA linear EST 06-AUG-2001		

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                                                                                                                                                                                                                                          603 CAATTGTTGATAAAGGGAGAACAAAATATGTTGINNNNNNNNNNNNNCCITCCTGIACCA 661
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/dev_stage="Embryonic (d12,d14,d19); post hatch (w1,w3,w5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="pgplc.pk002.al3"
/clone_lib="Primary Chicken Pituitary/Hypothalamus/Pineal
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RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Inpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Riken integrated sequence analysis (RISA) system--484-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000) Ronno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
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Tel: 81-45-503-9222
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1-7-22 Suehiro-cho, Tsurumi ka, Yokohama, Kanadawa 230-0045, Japan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
(bases 1 to 634)
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                               prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Scuter and Genome Science Laboratory
                                                                                                                                                                                                                  primed with a primer [5] GASASASASASESSACIOSAGITTTTTTTTTTTTTTTTTTVN ()], CDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissuc_type="oviduct"
/dev_stage="2 days pregnant adult"
/lab_host="DH108"
was cleaved with BamHI and XhoI. Vector: a modified
                                                                                                                                            transcriptase and subsequently enriched for full-length by
                                                                                                                                                                                           grepared by using trobalose thermo-activated reverse
                                                                                                                                                                                                                                                                                                    contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                        RIKEN Division of Experimental Animal Research in Riken
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/~lone-"sp30024K22"
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                        Unpublished (2000)
Contact: Takao Isogai
                                                                                                                                                                                                                                                                                                                                                                                                              sequence.
   Genomics Laboratory
                                                                                HRI human cDNA project
                                                                                                                                           Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                                                                                                                                                                      Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.
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            Homo sapiens, Similar to beta-carotene 15, 157-dloxygenase, clone IMAGE: 4734856, mRNA.
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HBI haman cDNA project; 5'' & 3''.end one pass sequencing: Helix
Research Institute, cDNA library construction. Department of
Besearch Institute, cDNA library colonor iniversity of Tokyo, and
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Tel: 81-438-52-3975
Fax: 81-438-52-3986
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Contact: MGC help desk
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Tissue Procurement: CLONTECH
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1 (bases 1 to 974)
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(Dickson, Mark) mcd<sup>®</sup>paxil.stanford.edu
M , Schmutz, J., Grimwood, J., Rodriquez, A.,
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Marra,M., Hiller,L., Kucaba,T., Martin,J., Heck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Kitter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: custom primer used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Marra M/WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW04471
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314 286 1810
                                                                                                                                                                    injusted to a Dialli adaptor [TGTTGGCCTACTGG], digested and cloned into distinct Dralli sites of the pMELBS FLA vector (5' site CACCIGNGG, 3' site CACCATGG). What should be used to isolate the cDNA insort. Size selection was performed to exclude fragments (Likb, Eitharry constructed by Dr. Sumio Sugane (University of Takyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTCTGCCTCAAAACCTGCG and 3' end primer CTCTGCCTCAAAACCTGCG and 3' end
                                                                                                                                                 sequencing: 5' end primer CTTO primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="adult"
/lab_host="DH10B"
/lab_host="DH10B"
/notc-"organ: kidney; Vector: pME18S-FL3; Site_l: Inall1
/notc-"organ: kidney; Vector: pME18S-FL3; Site_l: Inall1
(CACTGTGTG); Site_2: brall1 (CACCATGTG), 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
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/db_xref:"taxon:10090"
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             Email: genome-resagsc.riken.go.jp,
URI:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,K., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okaraki,Y., Muramatsu,M. and Hayashızakı,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
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Arakawa, T. Carninci, P., Fukuda, S., Furuno, M., Hanagaki, I., Hara, A., A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, P., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuxi, H., Tagami, M., Tagawa, A., Takahasi, F., Takeda, Y., Tanaka, T., Toya, T.,
                                                                                                                                                                                                                               Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagiwa 230-0045, Japan
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                           Unpublished (2001)
On Aug 1, 2000 this sequence version replaced gi:9637214
Contact: Yoshihide Hayashizaki
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Muramatsu,M. and Hayashizaki,Y. RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
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  Fujiwake,S.,
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     Inoue, K.,
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  lzawa,M., ⊖hara,E
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1160 TEGAAGTGAAGAAGAAGATTAOOTOOATOOCAAGCEGOAAGCGCTTEGTEGTGTGTGTGTGT 1219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             980 TTCACTTTGTAGACAGAAAGACGAAAAAAAAGAAGTATCCACCAAGTTTTACACTGATGCTT 1039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 TTCATATOATOONOONAAGGACCAGGAAGCCTGTGCGTTACCAAGTTCTACACACAATCCCA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library Genome Ros 11 (2), 291-299 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Alzawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Division of Experimental Animal Research in Riken contributed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Computer-based methods for the mouse full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIKEN integrated sequence analysis (PISA) system--384-format
                                                                                                                                                                                                                                   TEGGCTACAGAGAGAATAGCTTGTACGATAT SETEFACTTAAAAAAAAACTGGAACAAAGACT 1159
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                                                                                                       TOGOCTATGAGGACAGCAGCCTCTATCAGCT TTTCTATCTGGGCTAACCTGAACAACAACGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        primed with a primer [5'
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/dev_stage="2 days pregnant adult"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="F230024K22"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="female"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clark,M., Johnson,Š.I., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy,S., Hiller,L., Kucaba,T., Marrin,J., Beck,C., Wylie,T., Underwood, K., Steptoe,M., Thelsing,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW078092 698 bp mrNA linear EST 07-c fe24d05.yl Zebrafish Washu MPIMG EST Danio terio cDNA clone IMAGE:4749785 57 similar to TH-Q4YGX2 g4YGX2 RPE65 PROTEIN
                                                                                                                                                                                                  info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and RessourcenzentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                      Matthew Clark, DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Genome Systems, St Louis Missouri (web address: www.genomesystems.com) (email contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Stephen L. Johnson Washington University School of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WashU Zebrafish EST Project 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryöta; Metazoa, Chördata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Danio rerio
                                                                                                                                                                                      www.rzpa.ae)
                                                                                                                                                                                                                                                                                                                                            CDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by:
                                                                                                                                                                                                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                        4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, HSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and Wilson, R.
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                                                                                                                                                             primer: T3 ET from Amersham
                                                                                                                                     quality sequence stop: 497
                                                                                                                                                                                                                                                                                                                                                                       zbrafish@watson.wustl.edu
                   /db_xref="taxon:7955"
/clone="IMAGE:3739785"
/clone_lib="Zebrafish WashU MPIMG
                                                                 /organism-"Danio rerio"
                                                                                                                  Location/Qualifiers
                                                                                            . 698
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Ostariophysi; Cypriniform
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Best Local Similarity 62.6%;
                                            451 GUCAAGGCATTUTUATACTTATCTUACACCAFLUCTGAGTTCACGGACAACTGCCTGATC 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          331 GTTTACTACAGAAGTAACTACCACCTCCGAAGTGACACATACAACTGCAATATAGAAGCAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211 TGGTTGCAAGGGGTACTTCTCCGAAATGGCCCAGGGATGCACACAATAGGGGAACACTAAA 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              271 TACAACCACTGGTTTGATGGCT1GGC1C1GCTGCACAGCT1CACGTTTAAAAATGGTGAA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     391 CGAATCGTGGTGTCTGAGTT1GGAACCATGGCTTATCCGGAFCCATGCAAAAAACATATTT 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 TACAGCCATTGGTTTGATGGAATGGCACTTTTCGCACAGTTTTTGCAATTAATAAAGGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 TGGGTGCAGGGAACACTAATACGCAATGGACCGTCTTGTTCTCTGTTGGAGAGACGACA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGCAGGCAGATERGATO FOR ATHABAAAAGCROTIGAGGCTGTGTGTGCACCCTGCTGCTGC
                                                                                                                                                                                                                             GAAAAAGAAAAGAAAICTIGITTIAAACACCIGGAAGIAGIAIGCICCAICCCTICI 810
                                                                                                                                                                                                                                                                                                             TGCATCGCGGAGAAGGGCATAACCAAATACATGTTGTTCAAGGTCC----
                                                                                                                                                                                                                                                                                                                                                                                     TCAATTGTTGATAAAGGGAGAACAAAATATGTTCTCTTTAAGATCCCTTTCTCTGTAGCA 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AACTIGGCAACIICTCACCCACACTAIGACAGTGCTGGAAATATTCTCAACATGGGTACT 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTGACCCTGTTACTTTAGAGACTCAGGAAAAGATTGACTACCTGAAAFACCTTCCTGTA 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTGATECACAGAGACTOTOGAGACACTAGATAAGGTAGACTACAGCAAATATOTAGCTGTA 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AACATAATCAAATATGGAAATGACTTCCATGCTACGTCTGAAACCAATTATATTCGGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>AGTATPSTEGSPTFOTCATACACACTATGACAAAGAGGGAAACAGCTACACTATGGGAACA</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  by Matthew Clark (Lehrach lab; ICRF, London and Max Planck
Institut tuer Molekulare Genetik, Berrin), cDNAs for EST
analysis were selected following oligonucloutide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: psport1: Site_1: Not1: Site_2: Sall: lst
strand cDNA was primed with a Not1: olido(dT))!5 primer
[5'psAcTAGTTCTASATCCCCAGCGCCCCCTTTTTTTTTTTTT7']:
double-stranded cDNA was lighted to Sal i adaptors (HRL)
digested with Not1 and cloned into the Not1 and Sal i
sites of the psport1 vector (RPL). Library was constructe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     were sequenced additional times to assess quality
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                                                                                                                    133 ATGGAGACAATATTTAACAGAAACAAAGAAGAAFOOAGAAFOOATAAAAAGCTGAGGTG 192
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606 bp mRNA linear EST 07-MAR-2002
Ly36h09.yl Sugato STr adult male Lanto regto cton clone Speci48 57
Similar to TR:Q9YGX2 Q9YGX2 RPE65 PROTEIN.;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Consortium/LLNL, send email to: info@image.llnl.gov
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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Contact: Stephen L. Johnson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a Draill adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG, Xhor should be used to isolate the CLNA
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/dev_stage="adult"
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/db_xref="taxon:7955"
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                                                                                                                                                                                                                                                                                                                                                                         found through the 1.M.A.G.E. Consortium/ILNL at: http://image.linl.gov plate: LLCM1598 row: k column: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
lissue Producement: CLONETECH (aboratories, Inc
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/clone="IMAGE:4734856"
/clone_lib="NIH_M3C_76"
/clone_lib="NIH_M3C_76"
/lab_host="DH1OB (T1 phage-resistant)"
/note="Urgan: liver: Vector: plnk-LIB (Clontech): Site_1:
Sfil (ggccgcctcggcc); Site_2: Sfil (ggccattatggcc); 5' and
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                                                                                Kohara,Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H. Medaka EST Project in Takeda's lab Unpublished (2001)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BJ487612 MEGIESA CDNA Gryzias latipes cDNA clone MEGIESAGGROJ4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryzias latipes
                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazca, Chordata, Craniata, Vertebrata, Euteleustomi; Actinoptorygii, Neupturygii, Teleustei, Euteleustei; Neuteleustei; Actanthomorpha; Acanthoptorypii; Percomorpha; Atherinomorpha; Acanthoptorygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyldae; Oryziinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
Email: tshini@genes.nig.ac.jp
                              Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Japanese medaka.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BJ487612.1 GI:22166361
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                                                                                                                                                                                                                                                                                                                      (bases 1 to 648)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188 3
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F61FSA003014 51,
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COMMENT

SOURCE KEYWORDS

ORGANISM

Homo sapiens Eukaryota; M

Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

BM717865.1 numan

DEFINITION ACCESSION

UI-E-EJO-ain-n-09-0-UI-r1 UI-E-EJO Homo sapiens cDNA clone UJ-E-EJO-ain-n-09-0-UI-s', mrNA sequence.

EST 01 MAR 2002

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 8.5%; Score 264; DB 13; Length 648; Best Local Similarity 65.6%; Pred. No. 8.le-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                         1072 GAAGATGGCCACGT-TGTTTTTGATAICGTTGCCTA 1106
                                                                                                                                                                                                                                                                                    613 GARGARGGCCARGREGGCROCHTGARGROAFIGCCTA 648
                                                                                                                                                                                                                 493 AAGITITTEEETGAGGAAAATACTETEAFECACCTGATAGAAAAAAAAAGCTGGAAAAAAG 882
                                                                                                                                                                                                                                                                                                       892 CIGGALAFIG FCAAACIGG TAACFGCCT ACA FCCGAGGIGIGAACT GGGCTT 951
                                                                                                                                                                                                                                                                                                                                                            373 TACTATCAGAGOTTGGGCATGACTGAAAACTACATCATCATTGAAGAGCCCTTTCAAG 4×2
                                                                                                                                                                                                                                                                                                                                                                                              832 TACTACCACACCTTTGCAATCACAGAAAATTATATTGTGTTCATAGAGAGGAGGCATTTAAA 891
                                                                                                                                                                                                                                                                                                                                                                                                                              7.53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     715 AAATATGTTCTCTTTAAGAICC---CTICCICIGIGCGAGAAAAAGAAAAGAAGAAGAAACT 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       475 CACACCATTUCTGACTICACGGACAACTGCCTGATCAACATTATGAAAACTGGGGATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  772 IGETERAAACACCEGGAAGIAGIATGCECCAECCEICECECCCCCCCCCCCCCAACCAAGC H31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           595 CTAGATAAGGTAGACTACAGCAAATATGTAGGCTGTAAACTTGGCAACTTGTCAGGCAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   535 TATTATGCTACCAGTGAGACTAACTTCATCAGAAAAATTGATCCACAGACTCTGGAGACA 594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 CACACTGTGCCCGATTTCACTGATAATGCTGCGAGCAACATCATCAAGTATGGGAATGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="mixture of female and
/tissue_type "whole embryo"
/dev_stage="iry_stage 40"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="MF01FSA003014"
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/db_xref="taxon:8090"
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                                                                                                                                                                                                                                                          1058 TAAATGCTTACGAAGAAGATGGCCACGTTGTTTTTGATATCGTTGCCTACAGAGACAATA 1117
          1178 TIACCICCATCCCAACCIGCAAGGGCTTTGTTGTGCCTCTGCAGTATGACAAGGATGCAG 1237
                                                                                                                                       1118 GCTTGTACGATATGTTTTACTTAAAAAAAACTGGACAAAGACTTTGAAGTGAACAACAAGC 1177
                                                                                                                                                                                                       121 TCAACGCCTAGGAAGAGGACGGCTGCATCGTGTTGACGTCATTGCCTAGGAGGACAACA 180
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                                                                                                                                                                                                                                                                                                                              61 GGATTAGGTAGCTTGTGCAGACCAAGTTTTACACAGACGCCATGGTGGTGTTCCCATCACG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGGCCTCCTGCCTGGCTTTCCACAGGGAGGGAGAGAGACTTATATCACACATCATCGACCAAA 60
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Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of lowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Sequencing by: Dr. M. Bento Swares, University of Towa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact. Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                          GCCTCTACCAGCTCTTCTACCTGGCCAACCTGAACCAGGACTTCAAGGAGAACTGCAGGC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecok I adaptor, digested with Not I, and cloned directionally into pTTT3-Pac vector. The oligonaries in the used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (d1)1% tail Ihe sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGATTAAGTG; retina, CGGTC, keina Foveai and Macular, GTCC, RPE and Chorold, ACCTA. This library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI)."
1 164 c 141 g 123 t 3 others
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/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1. EcoR I. Site_2. Not I,
UT-E-EJO is a subtracted cDNA library constructed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        optic nerve, retina, Retina Foveal and Macular,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="fetal and adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="UI-E-EJO-ain-n-09-0-UI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 261 6: DB 14: Length 592;
Fred No. 2 De-36,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: zbrafishewatson.wustl.edu
cDNA Library Arrayed by:
CDNA Library Preparation: Paymond Leo CDNA Library Arrayed by:
Matthew Llark. DNA Seguencing by: Masslington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact info@resgen.com) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clark, M., Johnson, S. L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., St-jelu-M. M., Theising R., Ali-n, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kehn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, P.
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fk25f00.yl debidfish fin day! regeneration Danio rerio cDNA 5' similar to TP-Q9YT25 Q9YT35 RPF65 PPOTEIN. :, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                            www.rzpd.de)
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/tissue_type="1 day fin regenerates"
/lab_host="E. coli XJOIR"
/note="Vector: pBK-CMV, Site_1. EcoRI, Site_2: Xi
/note="Vector: pBK-CMV, Site_1. EcoRI, Site_2: Xi
strand rinA primed with (AA)lDACTAGTCTCGAG(T)18,
                                                                                                                                    /organism="Danio rerio"
/db_xref="taxon:7955"
/clone_lib="zebrafish tin dayl regeneration"
/sex="mixed male and female"
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EST 22-MAR-2000

Site_2: XhOI; 1st CGAG(T)18, followed

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                                                                                                                               Clark,M., Johnson,Š.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy,S., Hillier,L., Kucaba,T., Martiu,J., Reck,C., Wylie,T., Underwood, K., Steptoe,M., Thoising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Hatvey,N., Schulk,R., Fitter,E.,
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653 bp mRNA linear EST 06-MAY-2002 tz79e07.yl Sugano SJD adult male Danio terio cDNA clone 5914836 5' similar to TR:Q9YGX2 Q9YGX2 PPE65 PPCTEIN ;, mPNA sequence.
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                    Contact: Stephen L. Johnson
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Washington University School of Medicine
                                                                                              and Wilson, R.
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                                                                                                                                                                                                                                                                                                 403
                                                                                                                                                                           463 TCATACTTATCTCACACOM FOCIGAGITOA/GGACAACIGCCTGATCAACATTATGAAA 522
                                                                                                                                                                                                                                                                                                                                                                                                             343 AGTAAGTACCTCCGAAGTGACACATACAACTGCAATATAGAAGCAAACCGAALCGTGGTG 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               582 TATGGAAATGACTTCCATGCTACGTCTGAAACTAATTATATTCGGAAAATTGACCCTGTT 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            342 HETGALGGAALGGCACLELLGCAGLELLGCAATTAATAAAGGAGAGGLGAGGTACAGG 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               282 ACACTAATACGCAATGGACCTGGCATGTCTCTCTCTCGGAGAGGACGACATACAACCATTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution information can be found through the L.M.A.G.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4444 Forest Park Parkway, Rox 8501, St. Louis, MO 63108, HSA
Tel: 314-286-1800
Fax: 314-286-1810
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                               ACTGGGGATGATTATTATGCTACCAGTGAGACTAACTTCATCAGAAAAAATTGATCCACAG 582
                                                                                                                                                                                                                                      TCGGAGATGGGGACCATGGCGTACCGGACCATGCAAAAACATATTCTCCAAAGTGATC 521
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148 c 145 g
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/clone="5914836"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AW128477
478 bp mrNA linear EST 07-JUN-2001 fel6d05.yl Zebrafish WashU MPIMG EST Danio rerio cDNA clone IMAGE 3739017 5' similar to TR:09YGX2 GYGX2 FFE65 PF0TEIN : mFNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1998)
Contact Stephen L Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Rescarch Genetics, Huntsville, Alabama (web address: www_resgen_com) (email contact: info@resgen_com) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Genome Systems, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Danio terio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: zbrafish@watson wustl edu
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WashU Zebrafish EST Project 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kohn,
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Actinopterydii; Neopterydii; Teleostei; Ostariophysi; Cypriniformes
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                                                                                                          Institut fuer Molekulare Genetik, Berlin). cDNAs for EST analysis were selected following oligonucleotide hybridization fingerprinting of arrayed clones from cebrafish late somitogenesis (26 ss), adult liver or embryonic shield stage (5.6 h) libraries Fingerprint data were used to computationally cluster cDNAs, and a single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single chones.
                                                                                                                                                                                                                                                                                                                                                                                                                               double-stranded cDNA was ligated to Sal I adaptors (API.), digested with Not I and cloned into the Not I and Sal I sites of the pSFORTI vector (BKL). Library was constructed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               control
                                                                                      were sequenced additional times to assess quality
                                                                                                                                                                                                                                                                                                                                                                                                       by Matthew Clark (Lehrach lab; ICRF, London and Max Planck
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/db_xref="taxon:7955"
/clone="IMAGE:3739017"
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Shibata, X. Itali, M., Aizawa, K., Nagarka S., Sasaki, N., Gammini, P., Konno, H., Akiyama, T., Nishi, K., Kitsunai, T., Tashi, C., H., Itoli, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Kashiwagi, K., Yamamete, H., Sakaguchi, S., Ikedami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Orawa, K., Tanaka, T., Matsuura, S., Kawai, I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AKULUMUE Adult retina cDNA, RIKEN full-length enriched library, clone:A930029L06:homolog to RETINAL PIGMENT EPITHELIUM-SPECIFIC
                                                                                                                                                                                                                                    Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and aubtraction of cap trapper selected cDNAs to prepare tall length cDNA ibraries for rapid discovery of new geness genome Mes. 10 (10), le17-1630 (2000)
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                         with BamHI and XhoI. Vector. a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end; Sall; 3' end; HamHI Host; DHIOB. Retina RNA was provided by Stefaro Gustincich (Department of Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA 02115, USA) whose assistance is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kawai, J., Shinaqawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Alzawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Koudo, S., Yamanaka, I., Saito, T., Okazaki, Y., Cojobori, T., Pono, H., Kasukawa, T., Saito, P., Kadota, K., Matsuda, H., Ashburner, M., Patalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsudo, Y., Nikajdo, I., Pesoie, G., Custon, Lewis, S., Matsudo, Y., Nikajdo, I., Pesoie, G., Custon, County, Lewis, S., Matsudo, Y., Nikajdo, I., Pesoie, G., Custon, County, Lewis, S., Matsudo, Y., Nikajdo, I., Pesoie, G., Custon, County, Casavant, C., Custon, C., Casavant, C., Casavant, C., Lewis, S., Matsudo, Y., Nikajdo, I., Pesoie, G., Custon, C., Casavant, C., Casavant,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of
gratefully acknowledged
                                                                                                                                                                                                                                                                                                                                                        to Rot = 458.8. Second strand cDNA was prepared with the primer adapter of sequence [5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Please visit our web site (http://genome.gsc.riken.go.jp/) for
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Fax:81-45-503-9216)
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640 ACTIVIVAVVCACACIATIATGACAGTGCTGGAAATAFICICAACATGGGTACIICAATTGTT 699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              463 CCAGTGGGAAGAGTTACTATGAGAGAGAGAGAGACTTTATGAGAAGATTAAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5%ii iJAGArTICTGRAGARACTARATAARRTARARRTACARCAARTATRTAGCTGTAAACTTIGGCA 639
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754 TTOAAGCCAFCTIATGTALACAGTETTGTTGTCTCTGACTCCCAACTATATCGTTTTTTGTGGAG 813	754	рb
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643 AAAAATTTTACAGTTGCCTACAACATTATTAAGATCCCTCCACTGAAAGCA 693	643	Db

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: IDENTIFICATION OF CONSENTAL STATIONARY NIGHT RETAININGS.

FILE PEFERENCE: 19693/2481
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PPIOR APPLICATION NUMBER: 60/103,219
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552 TOGAGOGOTCAOOOCAAATGAAAATGATGGGACTCTTTACAACATTGGTAATTG 611
                                         633 CITGGCAACHCTCACCCACACIALGACAGIGCIGGAAAIALICTCAACATGGGIACTIC 692
                                                                                                                                                573 TGATCCACAGAGTCTGGAGAGACTAGATAAGGTAGACTACAGCAAATATGTAGCTGTAAA 542
                                                                                                                                                                                                 432 GGTCTACCCAGTAGGGGAAGATTACTACGCCTGCACGGAGACCACCTTCATTACAAAGAT 491
                                                                                                                                                                                                                        453 CAAGGCATTCTCATACTTATCTCACACCATTCTCACGCACAACAACTGCCTGATCAA 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138 GETEACGGGCAGTETECTGCATGEGGAECGGGGCTCTTCGAGGTTTGGATCTGAACCATT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213 GYTGCAAGGGTACFTCFCCGAAATGGCCCAGGGAGGCACACAATAGGGGACACAAATA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198 FFACCACCFGFTTGACGGACAAGCCCTTCIGCACAAGFICGACFTTAAAGAAGGACACGT 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          273 CAACCACIGGITIGATGGCTIGGCICIGCTGCACACCTTCACCTTTAAAAATGGTGAAGT ++2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153 AAACAAAGAAGAACATCCAGAGCCCATAAAAAGCTGAGGTGCAAGGTCAGTTGGCCAGTTG 212
                                                                                                                                                                                                                                                                                                                                                                                                                                              393 AATOGTGGTGTOLGAGIFTGGAAGGATGGCTIATCCGGATCGAAAAAAAAAATATTEGC 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            258 CACCTATCACAGAAGGTTCATCCGCACCGATGCTTACGTCCGGGGCAATGACCGAGAAAAG
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                                                                                                                                                                                                                                                                                              CAGGTTTTTTTCTTACTT-----CCGAGGAGTGGAGGTCACTGACAATGGCCTTGTTAA 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTACTACAGAAGTAAGTACCTCCGAAGTGACACATACAACTGCAATATAGAAGCAAACCG 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/04545370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.5%; Score 264.8; DB 4; Length 1724; 52.1%; Pred. No. 5.5e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0: Mismatches 702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45;
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Patent No. 5573939

RESULT 3 US-08-200-807-1

Sequence 1, Application US/08200807

Ē Ξ Ş Ę 문 Ę Š 2 돌 Ϋ́ US-U8-200-807-1 SENERAL INFORMATION:

APPLICANT: A VIK, Class Olof, Eriksson, Ulf
TITLE OF INVENTION. Isolated Flutein Receptors, Antibodies Which
TITLE OF INVENTION: bind Thereto, Nucleic Acid Sequence Coding
Patent No. 5573939
TITLE OF INVENTION: Therefor, And Uses Thereof
NUMBER OF SEQUENCES: 5 Query Match 7.9%; Score 247; DB 1; Longth 2629; Best Local Similarity 51.0%; Pred. No. 4.5e-56; Matches 741, Conservative 0, Mismatches 715, Indels 45. INFORMATION FOR SEQ ID NO: APPLIMATION NUMBER 17,xxx,549
FILING DATE: 15-MAY-11992
ATTORNEY JACKET INFORMATION
NAME: HARSON, NO 5574939man D.
PEGISTRATION NUMBER 10,446 PEGISTRATION NUMBER: 40,446
REFERENCE/DOCKET NUMBER: 1.1D 280
TELECOMMUNICATION INFORMATION. SUFTWARE: Wordperfect CURRENT APPLICATION DATA: HYPOTHETICAL: ANTI-SENSE: I MOLECULE TYPE: PRIOR APPLICATION DATA: COMPUTER READANCE FORM: MEDTUM TYPE: Diskette, 5.25 inch, 360 kb storage COPPESPONDENCE ADDRESS. SHOUTENCE CHARACTERISTICS: LENGTH: 2629 bases STREET: JOPOLOGY: TELEFAX: CLASSIFICATION: FILING DATE: APPLICATION NUMBER - HS/114/200,807 OPERATING SYSTEM. COMPUTER: THM PS/2 COUNTRY. STRANDEDNESS: TELEPHONE: ADDRESSEE: 371 TTTTCTTACTT -----CCGAGGAGTGGAGGTTACTGACAAIGCCCTIGTTAAIATCTAC 424 460 TTCTCATACTTATCTCACACCATTCCTGAGTTCACGGACAACTGCCTGATCAACATTATG 519 150 GAAGAGCAIGCAGAGCCCAIAAAAGCIGAGGCGCAAGGICAGIIGCCCACTIGGTIGCAA 219 251 CACAGAM3611CATTOSCACTGA ISCITACISTACGGGCAATGACTGAGAAAAGGATCGTC 310 440 ARAGERANETANIN MININ <u>189 — тайты Аладетта астемерен Аларын Аларын Аларын Аларын Аларын Алтас — 189</u> 71 GAGGAACTATOOPPACOGEPPACAGOOPATGITACAGGAACOGGALCOCCTTTGGCTAACC 130 10022 New York City nucteic acid 805 Third Avenue (212) 688-9200 (212) 838-3884 IJSA linear Felfe & Lynch no CDNA to mRNA single PC-DOS Sde

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1376 AAAGAAACCTGGGTATGGCAAGAGCCTGATTCATACCCCTCAGAACCTATCTTTGTTTCT 1435
                                                                                                                                                                                                                                                                                                                                                                  1316 TATGGACTTGGCTTGAATCACTTTGTTCCAGACAGGCTCTGTAAGCTGAACGTCAAAACT 1375
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1573 CCAA---ATAAAGCACCCTTCCIACTCAICTIGGAIGCTAAAACATTCAAAGAATTCGC 1529
                                                                                                         1436 CACCCAGATGCCTTGGAGGAAGATGACGGTGTAGTTCTGAGTGTGGTGAGCCCTGGG 1495
                                                                                                                                                                                              1225 GACAAGGATGCAGAAGTAGGTTCTAATTTAGTGAAACTTGCAACTTGCACAACTAGCTGCAAATAA 1284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1174 AAGCTTACC------TCCATCCCAACCTGCAAGCGCTTTOTTGTGCCTCTGCAGTAT 1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1016 GAATTTGTTTATAATTATATTTTAGCCAATTTACGTGAGAACTGGGAAGAGGTGAAA 1075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          997 AAGACGAAAAAAGAAGTATCCACCAAGTITTACACIGATGCTTTGGTGCTTTTATCACCAC 1956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   836 TACATGGATTGTTTTGAATCGAATGAAACCATGGGGGTTTGGGCTTCATATTGCTGACAAA 895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             937 TGGGGCTTCCTGCCTTTTCCTTTCATAAGGAGGATAAGACGTGGTGTTLACTTTGTAGACAGA 995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                716 TTCAAGCCATCTTACGTCCATAGTTTTGGTTTGACTCCCAACTATATTGTTTTTTGTGGAG 775
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  776 ACACCAGTCAAAATTAATCTGTTCAAGTTTCTTTCTTCATGGAGTCTTTGGGGAGCCAAT 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            880 CAGCCATTTAAACTGGATATTGTCAAACTGGCAACIGCCIACA---TCCGAGGIGIGAAC 936
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08488305A Patent No. 5679772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (212) 838-38 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT. B vik, Claes Olot, Eriksson, Ult. Peterson, Per A. TITLE OF INVENTION: Isolated Protein Peroptors, Antibodies Whit TITLE OF INVENTION: bind Thoreto, Nucleic Acid Sequence Coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: OF HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION: NAME: KOLL, Vineet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.5 inch, 1.44 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity hes 791; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 37,003
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51 AACAGGAAAGATTTTTTTTAGTTTAGAGAGAGAGATATTGTATATTTTGTAGAGAGAGTT 110

Mismatches 167:

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US-08-232-463-14 pragpt-F1s
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                    Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                       TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                     REFERENCE; DUCKET NUMBER: 30 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            ATTOPNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
PEGISTRATION NUMBEF: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                       IMMEDIATE SOURCE:
                                                                                                                                                                                                SEQUENCE CHARACTERISTICS.
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCRRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1556 AGGGCTGAAGTGGAGATTAACATCCCCGTCACCITICAIGGACIGIICAAA 1606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1436 CACCCAGATGCCTTGFAGGAAGATGACGFGTAFATTCTGAGTGFGGTGGTGAGCCTGGG 1495
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                      Similarity
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conservative 214;
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26-AUG-1991
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                1.5%; Score 47.2; DB
4.8%; Pred. No. 0.014;
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NUMBER OF SEQ ID NOS: 544
SOFTWARE. FASUSEQ for Windows Version 3.0
SEQ ID NO 408
LENGTH: 588
TYPE: DNA
ORGANISM: Homo Sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                              Matches 128;
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CURRENT FILING DATE: 1999-08-30
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EARLIEP FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: 60/117,393
EARLIER FILING DATE: 1999-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ENDEGE, WILSON O., ET AL.
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS: II
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER: 60/098,639
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(588)
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                   1787 AAGAACAACCATATAACGACACAAAATGACTATGTATAAATCTCTTAAAATAATA-GATATA 1845
                                                                                                                                                                                                                        1727 CGACTACACAAACTGAGACAACTTTCTACTGAACATGAGTTAATATCCCTTTTTACCATTC 1286
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: Patent No. 5840070
: GENERAL INFORMATION:
: TOANT: ST. GEORGE-HYSLOD, PETER H
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บร-กห-จะ7-1ก1-2ห/c
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APPLICANT: Burmeister, Paula
APPLICANT: Delillo, Joanna
TITLE OF INVENTION: Pesticidal Proteins
FILE REFERENCE: MA703C2
CURRENT APPLICATION UNMERS: US/09/3/8,088A
CURRENT FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: US 08/633,993
PRIOR FILING DATE: 1996-04-19
FRIOR FILING DATE: 1997-04-18
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US-09-378-088A-81/c
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ZIP: 02110
CLMEDIUM TYPE: FLOPPY disk
CLMEDIUM TYPE: FROPPY disk
CLMEDIUM TYPE: IRM PC compatible
CLMEDIUM SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
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                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HORWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
                                                                                                                                                                                                                                             APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENERIC SECTENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                      COUNTRY:
                                                                                                                                                         CITY: Boston
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                                                                                                                                     Massachusetts
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                                                                                                                      U.S.A.
           Patentin Release #1.0,
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             Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-592-541-28/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
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APPLICANT: ST GET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                 ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 2307 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                            FILING DATE:
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                            CITY: Boston
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TELEPHONE:
                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                   COUNTRY.
                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: TESTA, HURWITZ & THIBEAGLT STREET: High Street Tower - 125 High Street
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(617) 248-7000
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US-09-124-698-28/C
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APPLICANT: ST. GEORGE-HYSLOP, PETER H

APPLICANT: ROMMENS, JOHANNA M

APPLICANT: FRASER, PAUL E

TITLE OF INVENTION: GENETIC SEQUENCES

TITLE OF INVENTION: TO ALZHEIMER'S DIS
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Matches 97; Conservative
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                                                                                                                       NAME: Pitcher, Edmund R.
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (617) 248-7100
TELEPAX: (617) 248-7100
INFORMATION FOR 519 (F NO: 29
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MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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TOPOLOGY: 11
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                                                                                                  SEQUENCE CHARACTERISTICS:
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                                                               TYPE: n
                                                                                                                                                                                                                                             FILING DATE
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CITY: Boston
                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/592,541
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                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                         FILING DATE
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High Street Tower - 125 High Street
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                       linear
  DNA (genomic)
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                                          single
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Pred. No. 0.22;
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US-09-127-480-28/c
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: Patent No. 6194153
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                                                                                                                                                                                                                                                                                                      NAME: Pitcher, Edmund R. TELECOMMUNICATION INFORMATION: (617) 248-7000
                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPOTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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APPLICANT: FRASER, PAUL E
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                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
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STATE: Massa
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                 1667 ATGRATGITTATACCACAGAATGATTTRACCGGTGAGACGGAATAAAACGCTAITSATC 1726
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                                                          Conservative
                                                                                                                                                                                                                             2307 base pairs
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                                                                                                                                                                          linear
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                                                                          1.3%; Score 41.8; DB 51.3%; Pred. No. 0.22;
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                                                        0; Mismatches
 DB 3; Length 2307;
                                                                                            DB 4; Length 2307;
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TELEPHONE: (212) 527-77:9
TELEPAX: (212) 753-6237
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 2307 base pairs
TYPE: nucleic acid
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                               y Match 1.3%; Score 41.8; DB 4; Length 2307;
Local Similarity 51.3%; Pred. No. 0.22;
thes 97, Conservative 0, Mismatches 52; Indeis 0
                                                                                                                                                                                                                 1667 AFGGGAFGITTALACCACAGAATGAATTTGGGGGCTGAGACGAAAAAAACGCTATTGAFC 1726
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NAME: Paul F. Fehlner, Ph.D.
REGISTRATION NUMBER: 35,135
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-TOS/MS-DOS
SOFTWARE: Patentin Pelease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMMRBH: US/08/496,841C
FILING DATE: 28-Jun-1995
                                              ZIF: 10022
COMPUTER READABLE FORM:
2033 ACCAAGACCCATATTACAAACCAATATGGTAACCTGTGTTCCCTTCTATGGTATGATTAT 1974
                                                                                             2093 CCAGAATCCCCATCCCCACAAAACTCATGGGAACAAAATTTAAAGGATAAAACAAAACCC
                                                                                                                                          1727 CGACTACACAAACTGAGACAACTTTCTACTGAACATGAGTTAATATCCCTTTTACCATTC 1786
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STATE: New Yor
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FRASER, PAUL E
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Parentin Pelease #1 0. Version #1 40
CURRENT APPLICATION DATA:
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MEDIUM TYPE, Fluppy
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COPPESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 2307 base pairs
                                                                                                                                                 2093 CCAGAATCCCCATCCCACAAAACTCATGGGAACAAAATTTAAAGGATAAAACAAAAACCC
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1973 GTCATGTTA 1965
                                  1847 TCCTTTTAA 1855
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FRASER, PAUL E
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                                                                                                                                                                                                                                                                                                           Conservative
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 Mismatches

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RESULT 14 US-08-980-060-3

US-09-307-185-3

; Patent No. 620

GENERAL INFORMATION:
APPLICANT: NI, JIAN

APPLICANT: NI, JIAN APPLICANT: FENG, PING

APPLICANT: MUZIO, MARTA
APPLICANT: DIXII, VISHYA M.
TITLE OF INVENTION: HUMAN IRAK-2
NUMBER OF SEQUENCES: 14
CORPRESPONDENCE ADDRESS:

Sequence 3, Application US/09307185

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RESULT 15
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APPLICANT: NI, JIAN
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INFURMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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APPLICANT: DIXIT, VISHVA M.
TIILE OF INVENTION: HUMAN IRAK-2
NUMBER OF SEQUENCES: 14
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                            R282 TATTCAGTGCGTATATATGTGAAAAGTCATGLTGCAAALCTTTCTGTGAAACAGATGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                           2946 TOTTTATARRI INAARIA IARAA AAA IARAA INTO TAAT DITAAT DITAATA DI AAAAA AA DI GOODE INTO TAAT DITAAT DI TAATA DITAAT DI TAATA DITAATA DI TAATA D
                                                                                                         3342 TTTTAAATTCACTGGGAGAATATCCTATTTAAAGTAATCTATAGTAATTTCTTTTTATA 3401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.3%; Score 41.2; DB 2; Length 3459; 53.0%; Pred. No. U.39;
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Search completed: July 15, 2003, 20:18:55 Job time: 140 secs
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NAME: STEFFE, ERIC K.
RAME: STEFFE, ERIC K.
RECISTRATION NUMBER: 36,688
RECISTRATION NUMBER: 1488.1010000/EKS/AJK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3459 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-307-185-3
                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                     Matches
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DUS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                            y Match 1.3%; Score 41.2, DB 4, Length 3459; Local Similarity 53.0%; Pred. No. 0.39; hes 88; Conservative 0; Mismatches 78; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.I.L.C. STREET: 1100 NEW YORK AVENUE, N W., SUITE 600 CITY: WASHINGTON STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/307,185 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                  3282 TATTCAGTGCGTATATATCTGAAAAGTCATGTTGCAAATCTTTCTGTGAAACAGATGCTA 3341
                                                                                                                                                                                                                                                                  2946 TCTTTATGGTTTTGCATGTATGAAGAATACACTGCCTAATTCTAATGTTAAAAAAGTCACTG 3005
                                                                              3342 TTTTAAATTCACTGGGAGAAATATCCTATTTAAAGTAATCTATAGTAATTTCTTTTTATA 3401
                                                                                                                                                                                                       3006 GGGTCAGATCTAGAGCTTAAGTAAGCAGTCTGGGGTTTTCAAATGTTTATATGTTCCATA 3065
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Minimum DB seq length: 0 Maximum DB seq length: 260000000
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//gn2_6/ptrodata/1/pubpna//ISO7_PIRCOMB.seq:*
//gn2_6/ptodata/1/pubpna//ISO8_NEW_PUB.seq:*
//gn2_6/ptodata/1/pubpna//ISO8_NEW_PUB.seq:*
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Copyright (c) 1993 - 2003 Compuges Ltd
                                                                                                                                                                                                                                                               /rgn2_6/ptodata/1/pubpna/HSn7_NEW_PUB.seq.*
/rgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
/rgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
/rgn2_6/ptodata/1/pubpna/HSn6_PUPCOMR seq.*
/rgn2_6/ptodata/1/pubpna/PCTUS_PUPCOMR seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than ar equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

15 16 17 18	c 110 c 121 c 133	0 000	Result
41.8 41.8 41.8 41.6 41.6	42.2 42.2 42.2 41.8 41.8	3111 444 444 4325 822	score
 	11111	100.0 1.4 1.4 1.4	Query Match
5285 5650 70768 8693 3459	5046 8856 1410 2000	3111 3037 5689 2000 2000 267 588 11260	Query Match Length
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US-10-038-001-1 US-10-038-001-2 US-10-135-322-13 US-10-172-086-38 US-10-172-086-38	US-10-239-676-16 US-10-239-676-134 US-10-99-278-81 US-09-948-842A-3170 US-09-938-842A-3170	US-10-053-192 2 US-10-172-086-89 US-10-239-676-89 US-09-938-842A-4412 US-09-938-842A-4412 US-09-871-161-468 US-09-871-161-468 US-09-871-161-468 US-09-871-161-468	ID
Sequence 1, Appli Sequence 2, Appli Sequence 13, Appl Sequence 38, Appl Sequence 3, Appli	Sequence 159, Appl Sequence 159, Appl Sequence 81, Appl Sequence 81, Appl Sequence 170, App Sequence 102, App	Sequence 2, Appli Sequence 85, Appl Sequence 89, Appl Sequence 4412, Ap Sequence 4810, Appl Sequence 2860, Appl Sequence 20, Appl	Description

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Sequence 1, Appli Sequence 24, Appl Sequence 5, Appli Sequence 5, Appli Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appli Sequence 3, Appli Sequence 4, Appli Sequence 3745, Ap	Sequence 3, Appl Sequence 3814, Ap Sequence 3814, Ap Sequence 38 Appl Sequence 28, Appl Sequence 1, Appl Sequence 1, Appl Sequence 7505, Ap Sequence 2791, Ap Sequence 556, App Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 12, Appli

ALIGNMENTS

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US 10 163 192-2
Segment 2, Application 18/19053192
Publication No 18/00/0087336A1
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; TYPE: DNA
; GPGANISM: CHICKEN
US-10-053-192-2
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; APPLICANT: BACHMANN,
; APPLICANT: BRUGGER,
                                                                                                                                                                                                                                       wory match 100.0%, Scorp 2111; Nost Local Similarity 100.0%; Prod No 0; Matches 2111; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: RETA, RETA-CAROTENE 15,157-TO-XYCENASES. NUCLEIC ACID TITLE OF INVENTION: SEQUENCES CODING THEREFOR AND THEIR USE FILE REFERENCE: 8,84-CAROTENE 15,157-TO-XYCENASES,...
THE PREFERENCE: 18,84-CAROTENE 15,157-TO-XYCENASES,...
THE PROFESION APPLICATION SHAREF. US,15,057-3,152
CURRENT FILLING DATE: 2002-01-15
CURRENT FILLING DATE: 2002-01-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 103382.0 PRIOR FILING DATE: 1999-02-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: WYSS, Adrian APPLICANT: WYSS, Markus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 10
61 AGCTGTTTTTAGCCCAGAGAGGAGGGCTACGCCTSCAGGAGGAGCIGGGIAGAGGA 120
                                                                                                      FRIEDLEIN, Arno M
WIRTE, Gabriele M
WODGON, Wolf-Dietrich
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                                                                                                                                                                                                                                                      0; Mismatches 0; Indels 0; Gaps
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	del Vo	υγ	QY Db	Оy	db	QY Db	ОĄ	op OA	Qy	QУ	Qу	Qу	Оу	Qy Db	υφ	ОУ	ργ	Qу
	TTGTTGTGCACCACGACGACGACGACGACGACGACGACGACGACGAC	1141 AAAAAACTGGACAAAGACTTTGAAGTGAACAACAAGATTACCTCCATCCCAACCTGCAAG 1z00 	1081 CACGITGTTTTTGATALCGILGCCTACAGAGACAATAGCETGLACGATATGTTTTACTTA 1140 	1021 AAGTETTACACTGATGCFFFPAGFSCFFFAFCAGGACALAAATGCFFAGGAAGAAGAFGGC 1080 	961 AAGGAGMATAAGAGGTGGTTTGACTTTGTMGACAGAAAAGAGGAAAAAAAAAA	901 GTCAAACTGGCAACTGCCTACATCCGAGGTGTGAACTGGGCTTCCTGCCTTTCAT 960 	841 AGCTTTGGAATCACAGAAAATTATATTGTGTTCATAGAGGAGGGATGTAAACTGGATATT 900	781 CACCTGGAAGTAGGTCCATCCCTTGTCGCTCCCACCAAGCAAG	721 GTTCTCTTTAAGATCCCTTCCTCTGTACCAGAAAAAGAAAAGAAAG	661 AGTGCTGGAAATATTCTCAACATGGGTACTTCAATTGTTGATAAAGGGAGAACAAAATAT 720	01 AAGGTAGACTACAGCAAATATGTAGCTGTAAACTTGGCAACTTCTCACCCACACT	41 GCTACC	81 ATTCCTGAGTTCACGGACAGCTGCCTGATCAACATTATGAAAACTGGGGATGATTATTAT 5	421 GCTTATCCGGATCCATACAAAAACATATTTGGCAAAAGATTCTCATAGTTATGTCACACC 480 	TACACATATAAACTIGCAATATAGAAGCAAACCGGAATCGTGGTGTGTGAGTTTGGAACCATG	CTGCACAGCTTCACGTTTAAAAATGGTGAAGTTTACTACAGAAGTAAGT	241 CCAGGGATGCAGACAATAGGGGGACACTAAATACAAGGACGACTGGTTTGATGGCTCTGGGCTCTGGCCTCTGGCTGGCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTTGGCTCTGGCTTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTTGGCGGC	181 AAAGGTGAGGTGCAAGGTCAGTTGCCCACTTGGTAGGAAGGGTACTTCTCCCGAAATGGC 240
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Qy	Qy Db	Фb	Db VY	Dh Qy	Φb	מת את	Db	Qγ	Дb	Q y Db	Οy	Db Qy	qa	dd	Qy	ОУ	Оy	Qy Db
2341 AAACCAAGIACATATGGTTTTAIGFAGCATTCAAFTATACTTCAGTGCTATTCCATCCTA	2281 AGCAAACAGCACTTGCTTTGCTAATAACCCCATGGTGTATTTTTCTTTTTTATGATGA-GA-A 	5 E	161	101	041	بــر د	21	61	2 2	41	81	21 21	6 5	1501 ATCTTGTTCCCAGCCCGATGCAAGAGAAGATGAAGGTGTGTTTTGACCTBTGTT 	41	81	1321 ATATTATGTGAAGGGALAGAAN GOCLOGLGLGACLATGACTACAATGCCAAAAAATAC 	61 61

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. OTHER INFORMATION, chemically treated genomic DNA (Homo sapiens) US-10-172-086 8^{\rm o}
                                                                                                                                                                                                                                                                          US-10-172-086-89
Sequence 89, Application US/10172086
Publication No. US20030113750A1
GENERAL INFORMATION:
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                                                                                                                    SEQ ID NO 89
LENGTH: 3037
 Query Match
                                                                                                                                                                                                            APPLICANT: Epigenomics AG IIILE OF INVENTION. Method and nucleic acids for the differentiation IIILE OF INVENTION: of prostate tumors
                                                                                                                                                                        CURPENT APPLICATION NUMBER: US/10/172,086 CURRENT FILING DATE: 2002:06:13
                                                                                                                                                     NUMBER OF SEQ ID NOS: 116
                                                                                                                                                                                                         FILE REFERENCE:
                                                                   FEATURE:
                                                                                ORGANISM: Artificial Sequence
                                                                                                      TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3001 CACTGGGGTCAGATCTAGAGCTTAAGTAAGCAGTCTGGGGTTTTCAAATGTTTATATGTT
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AAACCAAGTACATATGSIITISATGSAGSATTCAAATTATASTITCAAGGCTATTCCATCCTA 2400
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Score 46.4;
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; LOCATION: (3724, 3742 4743, 4755...4755, 4759
US-10-239-676-89
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Matches 117; Conservation
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APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION Diagnosis of Diseases Associated with Gene Regulation
FILE REPERENCE: 5013.1003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEC ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRICE FILING DATE: 2001-04-06
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DE 10019058.8
DE 10019173.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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2000-09-01
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                                                                            2362 AIGIAGCAFTCAAFIAFACEECAGEGTATECCAEGTIAAGCIIAIAAGCAATTTGTATT 2421
                                                                                                                                                                                                                                        2066 AGATGGTGTATTTAGGGTTGTAGGAATTTTGGTTGTATTCGAIGTATTACGGGGTTGCGT
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                                 2482 STCTAAAGATGAACAGGAATGTATCTTTTAITAGTAFIGFFAAFFGFFFACHALA 2538
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TAAATCAGTTTTCCTTGAGAATATCTGACATAACATTTTGTGTGTAATGAGATGACTATGTT 2481
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GENERAL INFORMATION:
APPLICANT: Budworth,
APPLICANT: Brown, [
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; Patent No. US20020144047A1
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APPLICANT: Budworth, P.
APPLICANT: Brown, D.
APPLICANT: Chang, H.
APPLICANT: Zhu, T.
APPLICANT: Wang, X.
APPLICANT: Wang, X.
APPLICANT: Cooper, Bret
TITLE OF INVENTION: Promoters for regulation of plant expression
FILE REFERENCE: 1360.001US1
CURRENT APPLICATION NUMBER: US/09/887,576
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SEQ ID NO 4412
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    1.4%; Score 44.2, DB 9, Length 2000;
Best Local Similarity 47.7%; Pred. No. 1.1;
Matches 159; Conservative 0; Mismatches 173; Indels 1;
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PRIOR APPLICATION NUMBER: 0S 60/213,848
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 0S 60/214,087
PRIOR FILING DATE: 2000-06-23
PRIOR PILING DATE: 2000-06-23
PRIOR PILING DATE: 2000-12-29
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEO ID NOS: 875
SOFTWARE: Past SEQ for Windows Version 4.0
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SEQ ID NO 2860
LENGTH: 267
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Best Local Similarity
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LENGTH: ZUUU
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                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kalos, Michael D. APPLICANT: Lodes, Michael J. APPLICANT: Persing, David H. APPLICANT: Hepier, William T. APPLICANT: Jiang Yogiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 159; Conservative
                                                                                                                                                                                                                                                               FILE REFERENCE: 210121.566
COMPENT APPLICATION MIMPEP: US/10/060,036
COMPENT FILLOS THEE: 2002-01-30
NUMBER OF SEQ ID NOS: 4560
                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF PANCPEATIC CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Benson, Darin R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               la nga aya jaboye
                      NAME/KEY: misc_feature
LOCATION: 196, 259, 266
OTHER INFORMATION: n + A,T,C or G
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ORGANISM: Arabidopsis thaliana
                                                                                                         FEATURE:
                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                           TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2516 TATTGTTANTTGTGTTACTACTATGCATTGCATTGAATGAGAGGCAATGTATTTGTAGGAGA 2575
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Query Match

Score 43.5;

; 6, BC;

Length

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US-10-239-676 20/c
; Sequence 20. Application US/10239676
; Publication No. US20030082609A1
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GENERAL INFORMATION:
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                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/098,639 FPTOR FILING DATE: 1996-08-31 NUMBER OF SEQ ID NOS: 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ENDEGE, WILSON O., ET AL.
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS: II
FILE REFERENCE: CODNA-260XX
  APPLICANT: OLEK, Alexander APPLICANT: PIEPENBROCK, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for windows Version 3 0
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Local Similarity 50 88;
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                                                                                                                                                                                                                                1906 AACTATTCCAAA 1917
                                                                                                                                                                                                                                                                                                                1846 ATCCTTTTAAGGCACAGCGATGAGTTTTACTACAGGTAAGGATATGGGAGAGTGGCATAT 1965
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                                                                                                                                                                                                                                                                                                                                                     344 ATATTCTCTATA 355
                                                                                                                                                                                                                                                                      284 GTCATGTTACCTTAGTGTTAAAAGATTAACATAAGGAAACTGCAGCAATATATAAAAAGAT 343
                                                                                                                                                                                                                                                                                                                                                                                                                                           164 CCAGAATCCCCATCCCCACAAAACTCATGGGAACAAAATTTAAAGGATAAAAACAAAACCC
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SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 150;
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TillE OF INVENTION. Libanosis of Diseases Associated with Gene Regulation FILE REFERENCE: 5013.1003
CHERENT APPLICATION NUMBER: HSZINZ239,676
CURRENT FILING DATE: 2002.09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER - POT/EPO1/03468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THER INFORMATION: Themically treated geromic DNA (Homo sapiens)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORCANISM: Artificial Sequence
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9561 TATCTCTTTAATAAAATCATCTATTIA 9534
                                    2597 TTTCTGTAGGTGAAAATGCATTTACTGA 2624
                                                                                  9621 AAAATCATATTTTAAAYTTTTCATAATATTTAAACTTTAAATTACCCCAAATTTACCTAATC 9562
                                                                                                                           2537 TACTATECATATGAATGAGAGGAATETACTFOTAGGAGAACFOAGATATACATTOAACAA 2596
                                                                                                                                                                       2477 ATGTTGTCTAAAGATGAACAGGAATGTATCTTTTATTAGTATTGTTAATTGTGTTACTAA 2536
                                                                                                                                                                                                                                                           2417 GTATTTAAATCAGTTTTCCTTGAGAATATCTGAGATAACATTTTGTGTGTAATGAGATGACT 2476
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Pred. No. 6.2;
0; Mismatches 178;
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RESULT 9
US-09-918-995-23852
US-09-918-995-23852
Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED TITLE OF INVENTION: FROM VARIOUS CONA LIRPAPIES FILE REFERENCE: 20411-756
CUMPRENT APPLICATION NUMBERO "15/09/018,095
CHERRIT FILING DATE: 2001-07-0
PRIOR FILING DATE: 199-01-20
PRIOR FILING DATE: 199-01-20
PRIOR FILING DATE: 199-01-20
SEG IL NO 238E2
LENGTH: 478
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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: OTHER INFORMATION: n = A,T,C or G
US-09-918-995-23852
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US-10-239-676-16
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APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013.1003
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Publication No. US20030082609A1
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LENGTH: 6046
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PPIOR FILING DATE: 2001-04-06
2000-04-06
2000-04-07
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CUPPENT FILING PATE: 2002 09 24
PRIOR APPLICATION NUMBER: PCT/EP01/03968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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DE 10019173.8
DE 10032529.7
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                                          2469 AGATGACTATGTTGTCTAAAGATGAACAGGAALGTALCTIFTAFTAGTATTGTTAATTGT 2528
                                                                                                                                                                                                                                                                                                                                                            2352 ATATGGTTTTATGTAGCATTCAATTATACTTCAGTGCTATTCCATCCTAATGTTATAAGC 2411
2589 TTCAACAATTTCTGTAGGTGAAAATGCATTT 2619
                                                                                    2529 GTTACTAATACTATGCATATGAATGAGAGCAATGTATTTCTAGGAGAACTCAGATATACA 2588
                                                                                                                                 2873 AATTTAIGTTAATTAAATTTATATTTTTTGAATATATGTAATAAATTTAIGTGGATAA1T 2932
                                                                                                                                                                                                                                                                  2412 AATTT GTATTTAAATCAGTTTTCCTTGAGAATATCTGACAIAACAIFITGTGFAAIG 2468
                                                                                                                                                                                                                                                                                                                  3084 CCATAATAAAAAAAAAAAAAAAAAAAAA 3111
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                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                1.4%; Score 42.2; DB 9; Length 6046; 49.8%; Pred No. 7.4;
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Дb
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Best Local Similarity
Matches 227; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 228 SEQ ID NO 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: OLFK, Alexander
APPLICANT: PIEPENHROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013.1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PCI/EPOI/03968
DE 10019058.8
DE 10019173.8
DE 10032529.7
DE 10043826.1
PRIOR PILLING DATE: 2001-04-06
2000-04-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DAIL: 2002-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: unsure LOCATION: (5595, 5601)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: unsure LOCATION (5449,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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2000-06-30
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1962 TCACALLCACCCACALAAALLECLACCICLAAAAAICTATTAAATTTAAATTACATTCIC 1904
                                           2534 TAATACTAFGCATAFGAATGAGAGCAAFGFAITFCLAGGAGAACICAGAFAFACALLCAA 2593
                                                                                           2419 ATT----TAAATCAGTTTTCCTTGAGAATATCTGACATAACATTTTGTGTAATGAGA1G 247+
                                                                                                                                                                                                                                                                                         2359 TETTATISTRAGGATTICAATTATACTTICAGTGCTATTCCATCCTAATGTTATAAGCAATTIGT 2418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2320 AATTATACTAAAAAATTTCTAAACAAATAATAATAATAAACAAAAACAATTTTAAAATTTAT 2261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2179 ATTCATACCAATGCATTTTCTTGGTGCTCGATTTACACTATAACCAAACTTAACTATTAC 22+H
                                                                                                                                         2474 ACTATGTTGTCTAAAGATGAACAGGAATGTATCTTTTATTAGTATTGTTAATTGTGTTTAC 2544
                                                                                                                                                                                                                                                                                                                                                                                       2200 -- AAACTAATTACATACTATTTATTCCTATAAAAAACAAAAACCAATACAAAAACCAAACTTT 214+
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2260 AACCAATTACTTTCAAATCCTAATTCACAAACATACTTATCTTACAAACAAATATTCAAT 2201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3053 TGGTAGTATTATTATTTAATTATTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.4%; Score 42.2; DB 9; Length 8866;
45.7%; Pred. No. 9.6;
vative 0; Mismatches 263, Indels 7
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                                                                                                                                                                                                                                                                                                                                       Sequence 3176. Application US/09938842A
Patent No. US20020150378A1
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Best Local Similarity 77.3%;
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COMMENT APPLICATION NUMBER: US/09/938.842A CHEPENT FILING PATE 2001-08-24 PRIOR APPLICATION NUMBER: US 60/227,866 PRIOR APPLICATION WIMBER: US 60/264,647 PRIOR APPLICATION WIMBER: US 60/264,647 PRIOR FILING PATE: 2001-01-16
                                                                                                                                             APPLICANT: Harper, Jeff
APPLICANT: Kreps. Joel
APPLICANT: Kreps. Joel
APPLICANT: Wang, Yun
APPLICANT: Zhu, Tung
TITLE OF INVENTION: STRESS-PEGHATEN GENES OF PLANTS, TPANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
ELLE PEFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: US 09/378,088
PRIOR FILING DATE: 1949-08-20
PRIOR APPLICATION NUMBER: US 08/633,993
PRIOR FILING DATE: 1946-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dojillo, Joanna
TITLE OF INVENTION: Pesticidal Proteins
FILE REPERENCF: MA-703C2D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/099,278
CURRENT FILING DATE: 2002-06-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1074 ATTTGT 1069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1134 CGGATCCACTAGTAACGGCCGCCAGTGTGCTGGAATFCGGATFAGTTGCTTGATAGAGAGAGC 1075
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Schwab, George E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burmeister, Paula
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Michaels, Tracy E.
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 Mismarches

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SEQ ID NO 3170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 107, Application 08/09925301
Patent No. 0820020082308A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 181;
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Best Local Similarity 45.8%;
                                                                                                                                               Matches
                                                                                                                                                                                          Query Match
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CORRENT FILING DATE: 2001-08-10
PFIOR APPLICATION NUMBER: POL/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rosen et al. TIPLE OF INVENTION. Nucleic Acids, Francias and Actibodies FILE REFERENCE: PA106
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                                                                                                                                                                                                                                                                                                                                                              SEFTWARF: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ JD NOS: 1694
                                                                                                                                                                                                                                                              LENGTH: 2804
TYPE: DNA
OPGANISM: Homo sapiens
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                                                                                                                                     Local Similarity 51 48;
nes 97; Conservative
                                             1972 GAGGGAAGAGGAGAAGGTAACGGGAATATTTAATAGAATATAGATTTCTGAGCAAAT 2031
1727 CGACTACACAAACTGAGACAACTTTCTACTGAACATGAGTTAATATCCCTTTTACCATTC 1786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1531 TAATTGCCTTACATATGTGAAAGGCCATTGTACGAGTTGTTAATTTTATACACAAAAGGTT 1472
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                                                                                                                                          Score 41.8; DB 10;
Pred No 5.6;
0; Mismatches 92;
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Sequence 1, Application US/10038001
Publication No. US/0020187952A1
GENERAL INFORMATION:
APPLICANT: FRIMER, Kenneth E.
APPLICANT: POGUE, Gregory P.
APPLICANT: POGUE, GREGORY P.
APPLICANT: POGUE, GREGORY P.
TITLE OF INVENTION: VECTORS
FILE REFERENCE: 008010179CPUS01
CURRENT APPLICATION NUMBER: US/10/038,001
CURRENT APPLICATION NUMBER: US/10/038,001
CURPENT: FILLING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 09/505,477
PRIOR FILING DATE: 2000-02-16
NUMBER OF SEO ID NOS: 9
SOPTWARE: FUSING TO WINDOWS Version 4.0
SEO ID NO 1
LENGTH: 5285
TYPE: DNA
ORGANISM: Porcine circovirus
US-10-038-001-1
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Search completed: July 16, 2003, 00:03:50 Job time: 490 sees
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US-10-038-001-1
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Database :
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Copyright (c) 1993 - 2003 Compagen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIE

Result No		Query Match (Gogt), DR 15	[+dojt].	泵	11.	Description
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                                                                 AAY97314;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bota,beta carotene 15,15' dioxygenase protein, nucleic acids antibodies, useful for production of vitamin A from carotene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WP1; 2000-551036/51.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beta, beta-carotene-15,15-dioxygenase; vitamin A; beta-carotene; transformation; fruit; vegetable; developmental disorder; ophthaimological disorder, antibody, detection; quantification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       therapy of opthalmological disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treatment; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beta, Beta-carotene-15,15-dioxygenase
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                                                        250 OPFKLDIVKLATAY FRÖVNMASSLSFHARDER IWERFVÜRKIKKEVSIKFYTDALVLYHHI
                                                                                                                                                                                                        241 GPEKLIO VELATAY I ROVNWAYOLISE HEFOR I WEBEVOER TEKEVS IKEY I DALVILYHHI
                                                                                                                                                                                                                                                  ALISHBRITHSPERIKHERINA WANAAASAMAAHTETTEALIAALIAALAKAMAKAMAKAMA OOL
310 NAYEEDGHVVEDIVAYRDNSLYDMEYLKKLDKDEEVNNKLIS DEDGKREVVELGYDKDAE
                                                                                                                     181 DKGRTKYVLFKIPSSVPEKEKKKSCFKHLEVVCSIPSKSLLQPSYYHSFGITENYIVFIE
                                                                                                                                                                                                                                                                                       10 EEHPEPIKAEVQGQLPTWLQGVLLRNGPGMHTIGDTKYNHWFDGLALLHSFTFKNGEVYY 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                               DKGRTKYVLFKIPSSVPEKEKKKSCFKHLEVVCSIPSRSLLQPSYYHSFGITENYIVFIE
                                                                                                                                                                                                                                                                                                                                                                          EEHPEPIKAEVQGQLFTWLQGVLLKNGFGMHTIGDTKYNHWFDGLALLHSFFFKNGEVYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         506 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 506; D; Pred. No. 0;
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The present invention describes primer sets for synthesising 5602 of full-length cDNAs defined in the specification where a primer set occupies. (a) an oligo-dE primer and an oligonucle-otide complementary strand of a polymorheotide which complementary of the 5602 nucleotide comprises at least 15 nucleotides; or (b) a combination of a polymorheotide of the complementary strand of a polymorheotide of the complementary to the complementary strand of a polymorheotide which comprises a 5 end of a complementary strand of a polymorheotide which comprises a 5 end of complementary strand of a polymorheotide which comprises a 5 end of polymorheotide which comprises a 1 end sequence, where the combination of the specification of the specification of the specification of the primers are useful for such those defined in the specification of the specification. The primers are useful for such such and these defined in the specification and/or diagnosts of the attendantly of the proteins encounted by the full-length cDNAs. The primers also useful for the combination of the full-length cDNAs. The primers allow obtaining of the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Primer sets for synthesizing polynucleotides, particularly the $602 full-length cDNAs defined in the specification, and for the detection and/or diagrasis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAY-2000; 2000JP-0183767
09-JHN-2000; 2000HP-0241899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             full-length cDNAs -
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T, Wakamatsu A,
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                                                             antibodies. Nucleotides encoding all or part of loop are useful as grimers or probes for specific amplification and/or detection of the paper that encodes born for isolation of related sequences in other organisms, for describing both levels in humans (to identify subjects requiring without A supplementation) and for detecting unclations in the book gene. The nucleotide encoding book may also be used to transform cells, particularly plant cells, to increase their vitamin A concorrs (especially in fruits and vegerables) and in gene therapy of subjects who have mutated or deleted forms of the book gene and thas low vitamin A levels and susceptibility to developmental or ophthalmological disorders. Antibodies raised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH1 63.4 to AAH14742 represent human with sequences: AAF42445 to AAH14742 represent amino acid sequences: and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY97313 standard; Peptide;
                                                                                                                                                                                                                                                        Beta, beta-carotene-15,15'-dioxygenase (bCOD) is used for enzymatic conversion of beta-carotene to viramin A and for raising specific
                                                                                                                                                                                                                                                                                                            Example 3; Page 7; 37pp; English.
                                                                                                                                                                                                                                                                                                                                             therapy of opthalmological disorders
                                                                                                                                                                                                                                                                                                                                                           Beta,hera caretone 15,15% diewygendse protein, nucleie beide antibodies, useful fer productien ef vitamin A from caretone
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ophthalmological disorder, antibody; detection, quantification;
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                                                against book are used for detection/quantification of book in
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25; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plants. The transpende plants have improved nutritional quality or physiological condition and accumulate vitamin A aldehyde and can take up beta-carotene from the medium. Expression systems encoding beta-diox are useful in the study of beta-diox activity. Identification of cDNAs encoding beta-diox allows the physiological characterization of mammalian vitamin A meriabolism. Vitamin A production in crops and microorganisms can be achieved by transforming the organisms or crops
ABB71747 standard; Protein; 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypoptide Beta-diox specifically cleaves beta-carotene to form vitamin A aldehyde. Beta-diox is is useful for producing transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7; Page 86-87; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dioxygenase (beta-diox) protein that cleaves beta carotene to form vitamin A aldehyde, and polynucleotides encoding them useful for producing transgenic bacteria, fungi, plants expressing the polypeptide
                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                      with the CDNAS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a beta-carotene dioxygenase (beta-diox)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GREE-) GREENOVATION PFLANZENBIOTECHNOLOGIE GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-MAR-2000; 2000EP-0105822.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beta-carotene dioxygenase; beta-diox; beta-oaroteno; vitamin A aldebyde;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of a beta-carotene dioxygenase (beta-diox).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG62840;
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                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                       GTMAYPDPCKNIF 106
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                                                                                                                                                                                                                                                                                                                                                                                            516 AA;
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Pred. No. 0.00037;
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Best Local Similarity
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(ABB57737-ABB72072).
                                                                                                                                                                                                                                                                      23-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                         AAU04291 standard; Protein; 620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          550 PSEPIFVPSPD 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      453 PSEPIFVPSPD 463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           620 AA;
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lycopene; beta-apocarotenal; beta-ionone; apolycopenal; drain seed; corn; oil seed; palm; chick-pea; diagnostic; therapeutic; riboxyme; rethocidy/itamin A deficiency; beta-diox II; transpeni; mutrition; carotene/retinoid pathway, vitamin A aldehyde; retinoir acid; crop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL36176-ABL30511), expressed DNA sequences (ABL301840-ABL36175) and the encoded proteins
                                                                                                                                                                                                                                                                              Drosophila beta-carotene dioxygenase (Beta-diox I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 42033; 21pp + Sequence Listing; English
                                                                                                                                                                                       Beta-carotene dioxygenase; beta-diox I; Drosophila; beta-carotene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         capable of detecting 1000 or more genes from Drosophila. The invention is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent
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AAG62841
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                   screening of an expression library to identify nucleic acids encoding beta-diox II or the structure of functional domains. The transgenic fund, yeast, insect, animal or plant cells, seeds, tissues, or whole organisms have improved nutritional quality or physiological condition and accumulate important metabolites of carotene/relinoid pathways such as vitamin A aldchyde and retinoic acid, beta carotene from the medium. Expression systems encoding beta-diox II are useful in the study of beta-diox II activity. Identification of cDNAs encoding beta-diox I and II allows the physiological characterisation of mammualian carotene/relinoid metabolism. Vitamin A production in copps and microorganisms can be achieved by transforming the organisms or crops
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seeds, e.g. corn; oil seeds, e.g. Brassica seeds; edible seeds e.g. palm; edible seeds or seeds with edible parts e.g. chick-peas; potatoes, carrots, sweet potatoes, sugar beets, banana. The polypeptide is useful for diagnostic and/or therapeutic purposes and for preparing antisense or ribozyme type therapeutic agents and for detecting any abnormality of endogenous beta-diox II. The beta-diox II specific antisense oligonuclectides derived from the DNA sequence are useful for dose response studies in relevant models of retinoid/vitamin A deficiency during any stage of an organism's development. The nucleic acids are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    carolene dioxygenase (Beta-diox I). Beta-diox specifically cleaves beta-carotene and lycopene to form beta-apocatotenal and beta-ionone, and apolycopenals, respectively. The DNA is useful for transforming grain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            determining the presence or quantity of beta-diox II nucleic acid and determining presence and amount of beta-diox II The polypeptide is also useful for increasing or decreasing the amount of beta-diox II levels in a cell of tissue which can modify the level of vitamin A and other retholds. Antibodies are useful for studying beta-diox II localisation, recoming full bodies are useful for studying beta-diox II localisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated mouse, human, rebrafish beta caretene diexygenase (beta-diex II) protein that cleaves beta caretene and lycopene to yield beta-apocaretenal and beta-ionome, and apolycopenals, respectively—
                  AAG62841 standard; Protein; 620 AA
                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 6; 116pp; English.
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20-MAF-2000; EqqueP-0105822
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                                                                                                                                                                                                                                                                                                                                                       with the cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence represents the amino acid sequence of Drosophila beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GREE-) GREENOVATION PELANZENBIOTECHNOLOGIE GMBH
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                                                                                                                                                                        453 PSEPIFVPSPD 463
                                                                                                                                 550 PSEPIFVPSPD 560
                                                                                                                                                                                                                                                                                                            620 AA;
                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                           2.1%; Score 11; DB 22; Length 620;
LOO.0%; Pred No. 0.047;
                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                    0
                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                    0;
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X X X X X X X D X C X A
X X X X X X X X X X X X X A
                                                                                                                                                                                                                                                                                                         AAU04293
                                                                                                                                                                                                                                                                                                                              RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    guery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a beta-carotene dioxygenase (beta-diox) polypeptide. Beta-diox specifically cleaves beta-carotene to form vitamin A aldehyde. Beta-diox is is useful for producing transgenic plants. The transgenic plants have improved nutritional quality or physiological condition and accumulate vitamin A aldehyde and can take
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diaxyg-mase (b-fardiax) protein that eleaves beta carotene to form vitamin A aldehyde, and polynucleotides encoding them useful for
                                    lycopene; beta-apocarotenal; beta-ionone; apolycopenal; grain seed; corn; oil seed; palm; chick pea, diagnostic, therapeatic, ribozyme, zebratish; retinoid/vitamin A deficiency; beta-diox II; transgenic; nutrition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 manmalian vitardiox allows the physiological characterization of mammalian vitamin A metabolism. Vitamin A production in crops and microorganisms can be achieved by transforming the organisms or crops
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 up betarrarotene from the modium Expression systems encoding betarding are useful in the study of betardiox activity. Identification of cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Fig 6; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          producing transgenic bacteria, fungi, plants expressing the polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPT: 2001-441713/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Von Lintig J, Vogt K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W0200148162-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beta-carotene dioxygenase; beta-diox; beta-carotene; witamin A aldebyde;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-SEP 2001 (first entry)
                  carotese/retinoid pathway, vitamis A uldehyde, retinois asid, crop
                                                                                                       Beta carotene dioxygenase, beta-diox I, zebia-2, beta-carotene;
                                                                                                                                                                                                                                           AAU04293;
                                                                                                                                                                                                                                                                                    AAU04293 standard; Protein; 549 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   with the cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GREE-) GREENOVATION PELANZENBIOTECHNOLOGIE GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-MAR-1000, 1000EP-0105822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-DEC-2000; 2000WO-EP13144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of a beta carotene dioxygenase (beta diox).
                                                                                                                                                                                          23-0CT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSLR; AAH42155
                                                                                                                                                                                                                                                                                                                                                                                                                                        453 PSEPIFVPSPD 463
                                                                                                                                                                                                                                                                                                                                                                                            550 PSEPIFVPSPD 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11;
                                                                                                                                               beta-carotene dioxygenase (Beta-diox II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         620 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      00.0%; Pred. No. 0.047;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 620;
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Gaps

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                                                                                                                                                                                                                                Control system produces, sayar process and for preparing antisense or contribusions beta-diox II. The beta-diox II specific antisense or configuration of the preparing antisense or configuration of the proposed and for preparing antisense or configurations beta-diox II. The beta-diox II specific antisense or configurations beta-diox II. The beta-diox II specific actions are also constituted for an organism's development. The nucleic action are also cuseful as probes and as a guideline to define new PCR (polymerase chain configuration) primers for the cloning of substantially homologous DNA configurations of the presence or quantity of beta-diox II. The polypeptide is also configuration of the presence or quantity of beta-diox II nucleic acid and determining the presence or quantity of beta-diox II levels in configuration of a cell or tissue which can modify the level of vitamin A and other creating of an expression library to identify nucleic acids encoding beta-diox II or the structure of functional duamins. The transgenic configuration in the configuration of the physiological condition and accumulate important metabolities of carotene/retinoid pathways such configuration and accumulate important metabolities of carotene/retinoid pathways such configuration and accumulate important metabolities of carotene/retinoid pathways such configuration and accumulate and refined acid and beta-carotene or take up beta-
                                  AAY 97 312
                                                RESULT 10
                                                                                                                                                                 Matches
               AAY97312 standard; Peptide; 8
                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                           encoding beta-diox I and II allows the physiological characterisation of mammalian carotene/retinoid metabolism. Vitamin A production in crops an
                                                                                                                                                                                                                                                                                                                           as vitamin A aldehyde and retinoic acid, beta-carotene or take up beta-carotene from the medium. Expression systems encoding beta-diox II are useful in the study of beta-diox II activity. Identification of cDNAs
                                                                                                                                                                                                                                                                             microorganisms can be achieved by transforming the organisms or crops
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               apolycopenals, respectively. The DNA is useful for transforming grain seeds, e.g. corn; oil seeds, e.g. Brassica seeds, edible seeds e gralm; edible seeds or seeds with edible parts e.g. chick-peas; potatoes, carrots, sweet potatoes, sugar beets, banana. The polypeptide is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated mouse, human, zebrafish beta-carotene dioxygenase (beta-diox II) protein that cleaves bera carotene and lycopene to yield beta-apocarotenal and beta-ionone, and apolycopenais, respectively
                                                                                                                                                                                                                                                              with the cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and lycopene to form beta-apocarotenal and beta-ionone, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence represents the amino acid sequence of zebra-2, beta-carotene dioxygenase (Beta-diox II). Beta-diox specifically cleaves beta-carotene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Von Lintig J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GREE-) GREENOVATION PFLANZENBIGTECHNOLOGIE GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAR-2000; 2000EP-0105822
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                                                                                                                                                                               Local Similarity 100 0%;
                                                                                              111 NRIVVSEFGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-425657/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Fig 14; 116pp; English.
                                                                                                                                                               10;
                                                                                                                               NRIVVSEFGT 95
                                                                                                                                                                                                                                  549 AA;
                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vogt K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99EP-0125895
                                                                                                                                                                               1.9%; Score 10; DR 22; 00 0%; Pred No 0 43;
                                                                                                                                                               0: Mismatches
                                                                                                                                                               0,
                                                                                                                                                                                            Length 549;
                                                                                                                                                               Indels
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                                                                                                                                                             Gaps
                                                                                                                                                               0;
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                                                                                                                                                                                                                                                                                                                                                            ABG28616
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                                                                                                                                                                               RESULT 11
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food supplement;

Human; chromosome mapping; gene mapping; gene therapy; torensic; food supplement; medical imaging; diagnostic; genetic disorder.

Novel human diagnostic protein #28607

18-FEB-2002 (first entry)

ABG28616;

ABG28616 standard; Protein; 46 AA

1 AEVQGQLP

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Matches
                                                                                                                                      Query Match
                                                                       Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                             subjects requiring vitamin A supplementation) and for detecting mutations in the bCOD gene. The nucleotide encoding brop may also be used to transform cells, particularly plant cells, to increase their vitamin A contents (especially in fruits and vegetables) and in gene therapy of subjects who have mutated or deleted forms of the bCOD gene and thus low vitamin A levels and susceptibility to bCOD gene and thus low vitamin A levels and susceptibility to developmental or ophthalmological disorders. Antibodies traised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Buta, beta-carotene-15,15'-dioxygenuse (bCoD) is used for enzymatic conversion of beta-carotene to vitamin A and for raising specific antibodies. Nucleotides encoding all or part of bCD are useful as primers or probes for specific amplification and/or detection of the gene that encodes bCoD, for isolation of related sequences in other organisms, for determining bCOD levels in humans (to identify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beta, beta-carether 15,15°-diexymenase protoin, nucleic acids and antibodies, useful for production of vitamin A from caretene and denotherapy of opthalmological disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beta, beta carutene 15,15-dickytenase, vilamin A: beta carotene; transformation; fruit; vegetable; developmental disorder; ephthaimological disorder; antibody, detection, quantification;
                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treatment, therapy.
                                                                                                                                                                                                                                                                                                                   against bcob are used for detection/quantification of bcob in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Page 7; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-551036/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wyss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bachmann H, Brugger R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HOFF ) HOFFMANN LA ROCHE & CO AC F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1666T-833-77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03 JAN-2001 (first entry)
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18 AEVQGQLP 25
                                                                                                                                                                                                                 8 AA;
                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000EF-0102289.
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                                                                                                     1.5%; Score 8; DH 21; L
100.0%; Pred No 7 Re+OS;
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                                                                       د.
                                                                       Mismatches
                                                                                                                                          Length 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wyss A:
                                                                   Solpe
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В
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                                                                                                                                                                                                                                        RESULT 12
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II) (II) is useful for generating antibodies against it, determing or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note. The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensies, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
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                                                                                                                        31-JAN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; SEQ ID No 58975; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAS92803.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC
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                               treatment; uterine; gene therapy; expressed sequence tag
                                               Endometrium; human; tumour; cancer; anticancer; cytostatic; EST:
                                                                                  Human endometrium tumour EST encoded protein 354.
                                                                                                                                                                                                  AAY60294 standard; Protein; 82 AA
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                                                                                                                                                                                                                                                                                                                                  223 SIPSRELL 230
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                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                      100 08;
                                                                                                                                                                                                                                                                                                                                                                                      1.5%; Score 8; DB 22;
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                                                                                                                                                                                                                                                                                                                                                                      Mishatches
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RESULT 13
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Best Local Similarity
Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              that are highly expressed in uterine tumour tissue and which have anticancer and cytostatic activity. (A) are used (i) for recombinant expression of polypoptides (B) and (ii) to isolate complete genes. (B) are used (i) to identify agents suitable for treatment of uterine or endometrial cancer; (ii) directly for treating these forms of cancer (including expression from gene therapy vectors) and (iii) for
                                                                                                                                                                                        Canine, dog, kFE65, canine retinal pigment epithelium 65; KFE65; congenital stationary night blindness; CSNB; mutation detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       different parts of the same unknown dene, distorting the estimated frequency of occurrence in a particular tissue. AAY5941 Y60328 represent protein fragments encoded by the human endownettium tamour cDNA library duried EST fragments represented in AAC41281 242121.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         generation of specific antibodies. (A) are identified by assembling ESTS (expressed sequence tags) from a particular tissue type before comparison of expression patterns. This allows a significantly longer fragment of the gene to be revealed, so should reduce the number of failures assembled with the fast that ESTs from different libraries may represent assembled with the fast that ESTs from different libraries may represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              derived polypeptides, for treatment of all and identification of therapeutic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAZ42095
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05-OCT-1998;
                                                                                                                                      Canis familiaris
                                                                                                                                                                                                                                             Canine mutant RPE65
                                                                                                                                                                                                                                                                                                                                                       AAB/3955 Stabdard, Protein, 205
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                               रेश प्राप्त 1वदवः
                                                                                                    US6201114-B1
                                                                                                                                                                                                                                                                              29 MAY 2001 (first entry)
                                                                                                                                                                                                                                                                                                                    AAB73956;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a mutated version of canine retinal pigment epithelium 65 (PPE65). The gene encoding this protein contains an AAGA deletion at nucleotides 487-490 and is responsible for the disease congenital stationary night blindness (CSNB). The gene is useful for identifying drags which are genetically normal, or are carriers of, or affected with congenital stationary night blindness (CSNB). This allows a breeder to eliminate the carrier from the breeding stock or to breed
                                                                                                                                     25-FEB-1999;
05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acid molecule encoding canine retinal pigment epithelium 65, where presents of mutation in one or both alleles is indicative of a carrier of, or dog affected with congenital stationary night blindness
                                                                                                                                                                 25 FEB
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                                                                                                                                                                                                                    Arabidopsis thaliana.
                                                                                                                                                                                                                                     termination sequence
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99US-0156458.

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01-SEP-1999;

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PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1949; 99US-0161405.
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PR 26-OCT-1949; 99US-0161350.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0162142.
Query Match
Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 0; Gaps 0;

491 DAKTFKEL 498
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Db 126 DAKTFKEL 133

Search completed: July 15, 2003, 09:40:39

Job time: 74 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:
July 15, 2003, 09-40-45: Search time 43 Seconds
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Title:
Perfect score: 526
Sequence:
1 METIFNFNKEEHPEPIKAEV......MHLLLHGMFIPUNDLGAETE 526
Scoring table: 01100
Gapop 60.0 , Gapext 60.0
Searched: 283224 segs, 96134422 residues

Word size: 0
Total number of hits satisfying chosen parameters: 283224

Post-processing: Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Database · PIP_77.*
1: pir1:*
2: pir3:*
3: pir3:*
4: pir4:*

Pred. Not is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

A47143 pigment microsomal protein EPEKS, epithelium-specific become
RyAlternate names: membrane receptor p63; retinol-binding protein receptor
C:Species: Bos prinigenius taurus (cattle)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 05-Nov-1999
C:Cattle: 03-May-1994 #sequence_revision 03-May-1992 #text_change 05-Nov-1999
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RESULT 2 F81042

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C;Superfamily protein-tyrosine kinase axl; fibronectin type III repeat homology; :mmnnc
C;Keywords ATP, 41;***protein, phosphetransferase, tyrosine-specific protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein-tyrosine kinase (EC 2.7.1.112) brt - mouse C:Species: Mus musculus (house mouse) C:Date: 26.7ul-1946 *sequence_revision 26-7ul-1946 *text_change 94.Feb-2800 C:Accession: I58411
                                                                                                                                                                                                                                                                  F;501-778/Domain:
F;509-517/Region:
                                                                                                                                                                                                                                                                                    F:142-191/Domain: immunoglobulin homology <br/> <br/>KIN>F:501-778/Domain: protein kinase homology <br/> <br/>KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-856 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Status: preliminary; translated from GB/EMBL/DDBJ A:Molecule type: \mathtt{mRNA}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: brt, a mouse gene encoding a nawel receptor-type protein-tylosine kinase, A;Reference number: I58411; MUID:94150990; PMID:8108111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oncogene 9, 693-698, 1994
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A; Residues: 1-580 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Title: Complete DNA sequence of a serrgroup A strain of Neisseria menigitidis 22491.
A:Peterence number: A81775; MHID-20222555; PMID:10761919
A:Accession: A81989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P:Parkhill, J.; Achtman, M.; James, K.D.;
; Holroyd, S.; Jagels, K.; Leather, S.; Mc
Nature 404, 502-506, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable periplasmic protein NMA0687 [imported] - Neisseria meningitidis (strain 22491 C;Specles: Neisseria meningitidis C;Date: 05-May-2000 *sequence_revision 05-May-2000 *text_change 02-Feb-2001 C;Accession: AB1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB AL1f2753, GB.AL157959; NID:47379120; FIEN.CA683973.1, FID.4747941
A;Experimental source: serogroup A, strain Z2491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
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A;Experimental source: serogroup B, strain MC58
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K.; Leather, S.; Moule, S., Mungall, K., Quail, M.A., Rajandream
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                                                                                                              A; Molecule type: mRNA
A; Residues: 650-703 <LAI>
                                                                                                                                                                   A, Reference number: PT0183, A, Accession: PT0185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Title: Molecular cloning and in sity localization in the brain of rat Sky receptor A:Reference number: JC4166; MULD:96.104999; PMID:7490270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              K;Ohashi, K.,
J. Biochem <sup>1</sup>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ъ
A; Gene: tyro-3
                                C; Genetics:
                                                        C: Comment: This receptor plays an important role in development, function, and mainte
                                                                                A; Experimental source: sciatic nerve
                                                                                                                                                                                              Affitle: An extended family of protein tyrosino kinaso genes differentially expressed AfReference number: PT0183, MUID.9122566, FMID.2025425
                                                                                                                                                                                                                                                      R;Lai, C.; Lemke, G.
Neuron 6, 691-704, 1
                                                                                                                                                                                                                                                                                                                  A; Note: It is uncertain whether Met-1 or Met-7 is the initiator
                                                                                                                                                                                                                                                                                                                                          A, Experimental source, brain
                                                                                                                                                                                                                                                                                                                                                                     A, Cross-references | DDBJ.CX7880, NIO g1498195, PIDN BAAC7119.1, PID.4829057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.Date. 10 Sep 1999 #sequence_revision 10 Sep 1999 #text_change 16 Jun 2000 C:Accession: JC4166; PT0185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N.Alternate names, protein tyrosino kinoso sky mooghorotypo tyrosino kinoso rso
C:Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein-tyrosine kinase (EC 2.7.1.112) tyro3 precursor - rat
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., Honda, S., Ichinohiya, N., Nakamura, I., Mizuno, 117, 1267-1275, 1995

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C:Superfamily: protein-tyrosine kinase axl: fibronovin typo III ropost homology imm
C.Keywords ATF, diyo-protein, growth factor receptor, phosphotranstorase, tyrosine-s
E.43:105/Domain. immunoglobulin homology <1MMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: I49152; I48861
R;Schulz, N.T.; Paulhhac, C.I.; Lee, L.; Zhou, R.
Brain Res. Mol Brain Pcs. 28, 273-280, 1995
A;Title: Isolation and expression analysis of tyro3, a murine growth factor receptor A;Reference number: I49151; MUID:95240399; PMID:7723626
A;Accession: I49152
                                                                                                                                                                                                                                                                                       F:308-391/Domain: fibronectin type III repeat homology <3FK-
F:502-779/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Genetics:
A;Gene: tyro3; Etk2/tyro3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Status preliminary, translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues, 1.88 kRE2>
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A; Accession: I48861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R, Riesecker, L.G.; Giannola, D.M.; Emerson, S.G
Oncogene 10, 2239-2242, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C)Species: Mus musculus (bouse mouso)
C.Dato (2-Tul-1936 #sequence_recision 62 Jul 1996 #text_change 64 Feb 2000
                                                                                                                                                                                                                                                        F;510-518/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; introns:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A. Title: Identification of alternative exons, including a movel exon, in the tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:U18343; NID:q687627; FID::AAH26943.1; FID:q687628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-876 < RES>
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N;Alternate names, tyrosine kinase growth factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                 Matches
                                                                                                                                                                                    Query Match
                                                                                                                          local Similarity
les 8; Conserv
                                                                52 DGI,AI,I,HS 59
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DGLALLHS 243
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Pred. No.
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protein-tyrosine kinase (EC 2.7.1.112) tyro3 precursor mouse NyAlternate names: protein-tyrosine kinase sky; receptor-type tyrosine kinase rse; tyros C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Accession: B53743; S44141; JC2146; I49198; I49151, I48863; I48860
C; Accession: B53743; S44141; JC2146; I49198; I49151, I48863; I48860
R; Mark, M.P.: Scadden, D.T.: Wang, Z.; Gu, Q.; Goddard, A.; Godowski, P.J.
J. BBiol. Chem. 269, I0720-10728, 1994
A; Title: rse, a novel receptor-type tyrosine kinase with homology to Axl/Ufo, is express A, Petronne number, Asa744; MUID: 94193774; PMID: 7511503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RyPolvi, A.: Armstring, E.: Lai. C.: Lemke, G., Hurkber, K., Spills, F.A.: Guida
Gene 134, 289-293, 1993
Artitle: The human TYRO3 gene and pseudogram are located in chromosome 15g14-g25
A:Reference number JC2145; MP110:84085784, FW110:8262388
A:Accession: JC2146
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       A; Molecule type: mRNA
A; Residues: 7-880 - PE2 -
A; Cross-references: EMB
                                                                                                                                                                                    RESCHULT. N.T.: Paulhiar, C.I., Lew, L., Ebou, P. Brain Res. 108. Brain Res. 208. 209. 209. Aprille. Isolation and expression analysis of tyro3, a murine growth factor receptor tyros. Peference number: I49151; MUID:95240399; PMID:7723626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A:Title: Isolation of a receptor tyrosine kinase (DTK) from embryonic stem cells: struct A.Reference number. 149198: MUID:95161079; PMID:7857657 A:Accession: 149198
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R;Polvi, A : Armstrung, E : Lai, C : Lemke, G , Hurkber, K., Sprinz, F.A.: Guida, L :
Gene 134, 289-293, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A: Molecule type: mRNA
A: Residues: 7-629, 'F', F(1-8]:: 'V', 812-888 TLAIN
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F:214-299/Momain fibronectin type III repeat boundlogy: FN3A.
F:312-395/Momain fibronectin type III repeat boundlogy: FN3B.
F:312-395/Momain: transmembrane #$tatus fredicted iMM.
                                                                                                       A;Accession: 149151
A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DDBJ
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A; Residues: 1-880 < PES
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   EMBL: (18342) NIL): g687625, FION AAB26942 1, FIO. g687626
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R:Lai, C.; Gore, M.; Lemke, G.
uncogute 9, 2567-2578, 1994
A:Title: Structure, expression, and activity of Tyro 3.
A:Reference number: I48860; MUID:94736210; PMID:8058320
A:Accession: I48860
                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Mechanisms of Evolution in Biokettsia come it and Biokettsia prowazekii A;Peference number: A97700; MHID:21442074; PMID:11557893 A;Accession, A97719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein RC0153 (imported)
C.Species. Eickettsia conorii
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F;214-299/Domain: fibronectin type III repeat homology <FN3A>
F;312-395/Domain: fibronectin type III repeat homology <FN3B>
F;312-395/Domain: thansmembrane #status predicted <IMM>
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A:Residues: 7-579,10,531-819,707,812-880 /PE4>
A:Cross-references: EMBL:X78103; NID-9473096; PIDN-CAA54995 1: PID-9473097
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Oncogene 10, 2239-2242, 1995
Armitte: Identifiestion of alternative execs, including a movel exec, in the Cyrosine
Armeterine number, 148861; MULE 9530-4487; PMID 7784069
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                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A, Residues: 1.78 KERS
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Schenee 293, 2093-2095, 2001
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F;515-766/Domain. cytoplasmic tyrosine kinase #status predicted (CIK)
F;53,75,181,220,230,283,355,370/REnding site: correspyingte (Asn) (equalent) #status p
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A, Fesiones 1:92 - PE
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Best Local :
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54 LKKLDKD 60
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ative 0, Mismate
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A:Title: Complete Genome Sequence of Caulobacter crescentus. A:Reterence number. A87249; MUID:21173698; PMID:11259647 A:Accession: B87322
                                                                                                                                               R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durklin, A.S.; Gwind, M.L.; Haft, D.H.; Kolon n. J.: Ermolaeva, M.; White, O.; Salzberg, S.I., Shagiro, L., Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
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P:Hevan, M : Wedler, H : Wambutt, P : Banoroft, I : Mowes, H W : Mager, K F X : Schoolld
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awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;
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A; Molecule type: DNA
A; Residues: 1-125 <STO>
                                              A; Status: preliminary
                                                                                                                                                                                                                                                              C;Date: 20-Apr=2001 #sequence_revision 20 Apr 2001 #text_change 10-May=2001
C;Accession: B87322
                                                                                                                                                                                                                                                                                                                  chemotaxis protein CheYI [imported] - Caulobacter crescentus C_1Species: Caulobacter crescentus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Introns: 40/2; 92/3
A; Note: T805.60
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A; Residues: 1-124 <BEV>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Genetics:
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A:Title: Complete genome sequence of an aerobic hyper-thermophilic Grenarchaeon, Aeropyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein APE2498 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
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A;Accession: T05467
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A; Accession: B72482
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nes 7; Conservative (
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RESULT 12
H71197
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A;Molecule type: DNA
A;Residues: 1-177 <SAU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M., Olfuku, Y., Fanahashi, T., Tanaka, T., Kudah, Y., Yamazaki, J., Kushida, N.: Oqu DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper thermophili A;Reference number: A71000; MOID:98344137; PMID:9679194
A;Accession: H71197
                                                                                                                                                                                                                                                               C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable acetyltransferase - Streptomyces coelicolor
C.Species. Streptomyces coelicolor
C.Date. 05.Nov:1999 #sequence_recision 05.Nov:1999 #text_change 01 Jul 2008
C:Accession: T35580
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C;Superfamily: Pyromogous borikoshli bypothetical protein PH1854
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M., Ohfuku, Y., Funahashi, T., Tanaka, T., Kudub, Y., Yamazabi, J., Kushida, N.: Oqu
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C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 *sequence_revision 14-Aug-1998 *text_change 28-Jul-2000
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C, Superfamily, chemotaxis cheV protein, response regulator homology
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                                                                                                                                                                                                             C;Superfamily: Escherichia coli ribosomal protein-alanine N-acetyltransferase rimt
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                                                                                                                                                                                                                                                                                            A; Experimental source: strain A3(2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: Z21583
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T35580
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A;Experimental source: strain OT3
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A; Residues: 1-140 <KAW>
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Best Local Similarity 100.0%;
Matches 7; Conservative (
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hes 7; Conserv
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63 EEDGHVV 69
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                                                                                                        Conservative
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Pred. No. 44;
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A;Molecule type: DNA
A;Residues: 1-180 <MTH>
A;Fross-references: GB:AEDGORG: GR:AEQUURAN: NID:92622004; FION:AABB5415.1; FID:9262201
A;Experimental source: strain Delta H
C;Genetics:
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R.Smith, D.R.: Doucette-Stamm, L.A. Del-19thery, C., Lee, H., Dalvis, I., Aldredge, T., 101, D., Spadafola, R., Viraite, R., Wang, Y.; Wierzkowski, J., Gikson, R., Jiwani, N., Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
A.;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A. Reference number, A69000, MUID.98037514; PMID.9371463
A.;Accession: G69222
A. Molecule type: DNA
A. Status: preliminary; nucleic acid sequence not shown; translation not shown
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A;Rosidues: 1-181 <SCH >
A;Rosidues: 1-181 <SCH >
A;Cross-references: EMBL AL356173; GSPDB GNGGT16; N:SP:R1416 280
A;Experimental source: BAC clone B14D6; strain OR74A
C;Genetics:
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C:Superfamily: Methanosarcina barkeri molybdenum formylmethanofuran dehydrogenase chain
Search completed: July 15, 2003, 09:49:19 Job time: 45 secs
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                                                                                                                                                                                                                Best Local Similarity 100 0%; Pred. No. 56; Matches 7; Conservative 0. ""
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OM protein - protein search, using sw model
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Title: Perfect score: July 15, 2003, 09:31:10; Search time 25 Seconds
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Run on:

Sequence. 1 METIENRNKEEHPEPIKAEV MELDEHGMETPÓNILGAETE 526

Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112852

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Query Match 1.5%; Score 8; DB 1; Bost Local Similarity 100.0%; Pred. No. 3.4; Matches 8; Conservative 0; Mismatches

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AAMORERG 1: - piete proteome. AA: 42899 MW; biyFl075EB8F6115 CRC64;	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial or lines require a license agreement (one tip jown lefts) h, non-annotous send an email to license@isb-sib.ch).	The genome of Methanosarvina and Evalue for the effensive metabolic and physiological diversity."; Genome Res. 12.332.542 (2002). i. OMINITIO ACTIVITY: 2.ph.sph. F.gly. et al 2.3-dipb.spheglycerate. 3. phosphe-D-glycerate . 2.3-dipbospheglyceratei. SIMILARITY: RELONGS TO THE PHOSPHOGLYCEPATE MUTASE FAMILY. A-PGAM SUBPAMILY.	Zimmer A , Rarber P D , Cann I , Graham D E , Grahame D A , Guss A.M., Hedderich P , Ingram-Smith C , Kuethoer H C , Kreychi J.A., Leigh T A , I w , Liu J , Muthopathyy B , Peeve T N , Smith K., Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C., Ferry T C , Tarrell K F , Jing H , Macario A J.L., Paulsen I., Prichert M , Sowers K.P., Swanson R.V., Zinder S.H., Lander E., Mctcalf W.W., Birel B.,	SHOULENCE FROM N.A. SHOULENCE FROM N.A. SHAINN-2A / ATC: 35395 / DSM 2834; SHAINN-2A / ATC: 35397 / DSM 2834; SHAINN-2A / ATC: 35397 / DSM 2834; SHAINN-2A / ATC: 35397 / DSM 2834; Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,	15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Phosphoglycerate mutase (EC 5.4.2.1) (PGAM) (aPGAM). AFGM OR MA0132. AFGM OR MA0132. Methanosarcina acetivorans. Archaea; Euryarchaeota; Methanococci; Methanosarcinales; Methanosarcinaceae; Methanosarcina. NCBI_TaxID-2214;	RESULT 1 ADOM_METAC STANDARD; PRT; 397 AA. AC PS8812:

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TYO3_MC
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_MOUSE
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Mark M.R., Scadden D.T., Wang Z., Gu Q., Goddard A., Goddwski P.J.;
"RSE, a novel receptor-type tyrosine kinase with homology to Axl/Ufo, is expressed at high levels in the brain.";
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                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBI outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schulz N., Faulhiac C., Lee L., Zhou R., "Isolation and expression analysis of tyro", a murine growth factor receptor tyrowine kinase preferentially expressed in adult brain "; Brain Res Mol. Brain Res, 28:273-280(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95161079; PubMed=7857657;
Crosier P S , Lewis P M , Hall L R , Vitas M.R , Morris C.M.,
Beier D.R., Wood C R , Crosier K E ;
"Isolation of a receptor tyrosine kinase (DTK) from embryonic stem
cells: structure, genetic mapping and analysis of expression.";
Growth Factors 11:125-136(1994).
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01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tyrosine protein kinase receptor TYRO3 precursor (E° 2.7 1.112)
(Tyrosine-protein kinase RSE) (Tyrosine-protein kinase DTK) (TK19-2).
TYPPO3 OR DTK OR RSE.
                                                                                                                                                                                                                                                                                                                                                    Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine -
                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=BALB/c; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94336210; PubMed:8058320, Lai C., Gore M., Lemke G.;
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Mammalia: Eutheria: Rodentia: Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
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                                                                                                                                                           AXI/UFO SUBFAMILY.
SIMILARITY: CONTAINS 2 IMMUNOGIOBULIN-LIKE C2-TYPE DOMAINS SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                        tyrosine phosphate.
SUBCELLULAP LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: ABUNDANT IN THE BRAIN AND LOWER LEVELS
                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE TYP FAMILY OF PROTEIN KINASES.
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PROSITE; PS00109; PROTEIN_KINASE_TYP; 1
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00408; IGC2; 1. SMART; SM00219; TYTKC; 1
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SMART; SM00410; IG_like; 1.
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EMBL; U1893; AAC52148.1; ALT_INIT.
EMBL; U18342; AAB26942.1; ALT_INIT.
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Pfam; PF00069; pkinase;
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N-LINKED (GLCNAC...) (POTENTIAL).

PHOSPHOPYLATION (AUTO-) (BY SIMILARITY).

A -> R (IN REF. 3).

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IG-LIKE C2-TYPE DOMAIN 1.
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TYPOSINE-PROTEIN KINASE RECEPTOR TYRO3
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                                                                                                                                                                                                                                                                                           Prod. No. 7;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                          3H7AC35CBUI5B3F7 CEC64;
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01-007-1996 (Rel. 34, Greated)
01-007-1996 (Rel. 34, Last sequence update)
15-JHN-2002 (Pel. 41, Last annotation update)
Tyrosine-protein kinase receptor TYKO3 procursor (RC 2.7.1.112)
(Tyrosine-protein kinase SKY).

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Prodom: PDOCOON: Eukpkinase; 1
SMART: SMOCOGO, FN3 2
SMART: SMOCOGO, FN3 2
SMART: SMOCOGO, FN3 2
SMART: SMOCOGO; IGC2; 1.
SMART: SMOCOGO; IGC2; 1.
SMART: SMOCOGO; PROTEIN_KINASE_ATP: 1
PROSITE: PSOUND: PROTEIN_KINASE_TYP: 1
PROSITE: PSOUND: PROTEIN_KINASE_DOM: 1
PROSITE: PSOUND: PROTEIN_KINASE_DOM: 1
                                                    ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ohashi K., Honda S., Ichinomiya N., Nakamura T., Mizuno K., "Molecular cloning and in stim localization in the brain of rat sky receptor tyrosine kinase.";
J. Biochem 117:1267-1275(1995).
--- FUNCTION: MAY HE INVOLVED IN CELL ADHESION PROCESSES, PARTICULARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metaboa, Chordata, Crasiata; Vertebrata, Esteleostomi;
Mammalia; Eutheria: Rodentia. Sciurognathi: Muridae; Murinae: Rattus
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InterPro: IPR003600, Iy_like.
InterPro; IPR001245; Tyr_pkinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96104999; PubMed=7490270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegious (Rat)
              CARBOHYD
                           CARBOHYD
                                          DISULFID
                                                                                  BINDING
                                                                                               NP_BIND
                                                                                                              DOMAIN
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                                                                                                                                                                                                                                      SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000719; Euk_pkinase.
InterPro; IPR003961; FN_III.
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                                                                                                                                                                                                                                                  Immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AXL/UFO SUBFAMILY
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785
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ation; Transmembrane; Signal; Repeat;
                        BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLONAC.
N-LINKED
                                                                                                                        IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 2.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
                                                                                                            PROTEIN
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                                                                                  (BY SIMILARITY)
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(GLCNAC
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RESULT 4
RL9_CAEEL
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RESULT 5
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Best Local .
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InterPro; IPR000702; Ribosomal_L6.
InterPro; TPR000584; Ribosomil_L6_2
                                                                                                                                                                                                                                use by non-profit institutions as long a modified and this statement is not removed the removed the reput real lines requires a lineary agreement (Section send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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15-JUN-2002 (Rel. 41,
15-JUN-2002 (Pel. 41,
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Macri C., Vaudin M
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Khahdiridae: Peloderinae: Caenorhahditis
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                                                                                                                            SECUENCE
                                                                                                                                     Ribosomal protein
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                                                                                                                                                              Pfam; PPAA347; Pibosomal_Lb;
                                                                                                                                                                                                                                                                                                                                                   Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                    Submitted
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                                                                                                                                                                                                          EMBL; AC005679; AAK84469.1; -
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les 8; Conservative (
                                                         382 TAVKEKD 388
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YJFH_ECOLI

YJFH_ECOLT SIANFARD; PFT: 243 AA P39290; 01-FEH-1995 (Rel. 31, Created) 01-FEB-1995 (Rel. 31, Last sequence update)

243 AA

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InterPro; IPR001537; SpoU_methylase.
InterPro; IPR004441; rRNA_methyl_3.
Pfam; PF00588; SpoU_methylase, 1.
ProDom; PD001243; SpoU_methylase; 1.
TIGRPAMS; TTGP00186; rRNA_methyl_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-21156231; PubMed-11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Makino K., Ohnishi M., Kurokawa K., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001)
                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.; Welch R.A. Blattner F.R.; "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7. Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=0157:H7 / EDL933 / ATCC 700927;
STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINK=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III., Burland V., Mau B., Glasner J.D.,
Pose D.J., Mayhew G.F., Evans P.S. Ciroger J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E. T. Tavis N.W. Lim A., Dimalanta E.T., Potamousis K.,
                                                                                                                                                                                                                                                                                                                                      EMBL; U14003; AAA97076.1; -. EMBL; AE000440; AAC77137.1; -. EMBL; AE005651; AAG59376 1: -.
                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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STRAIN=0157:H7 / RIMD 0509952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Analysis of the Escherichia coli genome region from 92.8 through 100 minutes."; Nucleic Acids Res. 23:2105-2119(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blattner F.R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-K12 / MG1655;
MEDLINE=95334362, PubMed-7610040;
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Hypothetical tRNA/TRNA methyltransferase yjiH
YJFH OR B4180 OR Z5787 OR ECS5156.
                                                                                                                                                                  Complete proteome.
                                                                                                                                                                                    Hypothetical protein; Transferase; Methyltransferase;
                                                                                                                                                                                                                                                                                                                      EMBL; AP002568; BAB38579.1; -
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                                                                                                                                                            This SWISS PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by cor-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for communicati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Frenthee M.B., Sebalida M., Jannes K.D., Churcher C., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Gerdeno-Tarraga A.M., Chillingworth T., Cronin A., Davies R.M., Pavis P., Dougan G., Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M., Rutherfold K., Simmonds M., Skelten J., Stevens K., Whitehead S., Harrell B.G.; "Genome sequence of Yersin'a pestis, the causarive agent of plaque."; "Asture 413:523:527(2301).
                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-94222840; PubMed-Biotzio, Bergman T., Erickson K., Galyov E., Persson C., Wolf-Watz H.; Bergman T., Erickson K., Galyov E., Persson C., Wolf-Watz H.; "The lcrB (yscN/U) gene cluster of Yersinia pseudotuberculosis is involved in Yop secretion and shows high homology to the spa gene involved in Yop secretion and shows high homology to the spa gene involved in Yop secretion and Salmonella typhimurium.";
                                                                                                                     entities requires a freedom appropriat (i.e. http://www.or.send.an.email.to-licenseedsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                  J. Bacteriol. 176:2619-2626(1994).
-!- FUNCTION: COMPONENT OF THE YOP SECRETION MACHINERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES=Y pseudotuberculosis: STRAIN=YPIII; PLASMID pIBI; MEDLINE-94222840; PubMcd-8169210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ul-FEB-1995 (Rel. 41, Created)
Ul-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hu P., Elliott J., McCready P., Skowronski E., Garnes J., Korbayashi A., Brubaker B.R., Garcia E.; "Structural organization of virulence-associated plasmids of Yersinia pestis.".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES-Y.pestis: STRAIN-KIM5; PLASMID-PCD1;
MEDLINE-98427122: Fibmed-9746557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yersinia pestis, and
Yersinia pseudotuberculosis.
Plasmid pCD1, and Plasmid pIR1.
                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES=Y.pestis: SIKAIN=CC-92 / Biovar Crientalis: FLASMID-pCD1;
MEDLINE-21470413: PubMed=11586360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES-Y.pestis; STRAIN=KIM5; PLASMID-pCD1; MEDLINE-98422474; PubMed=9748454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yersinia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YOP proteins translocation protein T. YSCT OR YPCD1.46 OR Y0035.
                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO THE FLIR/MORE/SPAR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "DNA sequencing and analysis of the low Calt response plasmid pCD1 of
Yersinia pestis KIM5.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blattner F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perry R D
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               AF053946; AAC62558.1;
AL117189; CAH54923.1;
L25667; AAA27680.1; -.
                                                                             AF074612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diam't
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Straley S.C., Fetherston J.D., Pose D.J., Gregor J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EE-4611 4623(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                             AAC69785.1;
                                                                                                                                                                                                                                                                                                              Integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                              protein
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InterPro;

IPR002010; Bac_export

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ADD_RHILO
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                              Query Match
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           Matches
                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                        Kaneko T. Nakamura Y. Sato S. Asamizu E., Kato T., Sasamoto S. Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumo A., Mochicuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADD_RHILO
Q98GV2;
                                                                                                                                                                                                                                                   Mesorhicobium loti.";

PNA Res. 7:331-338(2000).

-!- CATALTTIC ACTIVITY: Adenosine + H(2)O = inosine + NH(3).

-!- SIMILARITY: RELONGS TO THE ADENOSINE AND AMP DEAMINASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase).
                                                                                           Hydrolase; Nucleotide metabolism; Complete ACT_SITE 186 186 POTENTIAL.
                                                                                                               Pfam; PF00962; A_deaminase; 1.
PF00917F, PS00485; A_DEAMINASE; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                              STRAIN=MAFF303099;
MEDLINE=21082930; FubMed-11214968,
                                                     SEQUENCE
                                                                                                                             Pfam;
                                                                                                                                                 EMBL; AP003001; BAB50114.1; -
                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                  Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhizobium loti (Mesorhizobium loti)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADD OR MLL3163.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00953;
                                                                                                                                    InterPro; IPR001365; A/AMP_deaminase.
                                                                                                                                                                                                                                                                                              "Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
          Local Similarity hes 7; Conserv
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                                                                                                                             PF00962;
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                                                   186
234
267
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324 AA;
           Conservative
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                                                     35247 MW;
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                  1.3%; Score 7; 1
100.0%; Pred. No.
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100.0%; Pred. N
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                                                   2411959E4E4F90EA CRC64;
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           Mismatches
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                              DB 1;
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RESULT 9
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Best Local
                                                                                                                                                                                                                                                                                 Matches
YG81_METJA
Q59075;
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SEQUENCE
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-!- FUNCTION. Catalyzes the formation of 5-methyl-uridine at position 54 (M-5-U54) in all trNA (By similarity).
-!- CATALYIC ACTIVITY: S-adenosyl-L-methionine + trNA = 5-adenosyl-L-homocysteine + trNA containing thymine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Kotchum K.A., Hood D.W., Peden T.F., Dodson R.J., Nelson W.C., Gwinn M.I., DoBoy R., Poterson J.D., Hirkey E.K., Haft D.H., Salzberg S.I., White O., Pleischmann P.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Riair E., Cittone H., Clark E.B., Cotton M.D., Interback T.R., Khouri H., Qin H., Vamathevan J., Cotton M.D., Interback T.R., Khouri H., Qin H., Vamathevan J., Gill T., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.P., Rappuoli R., Venter T.C.; "Complete genome sequence of Neisseria meningitidis serogroup B strain "Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=MC58 / Serogroup B;
MEDLINE=20175755; PubMed=10710307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
trNA (Uracil-5-)-methyltransferase (EC 2.1.1.35) (trNA(M-5-U54)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS01230; TRMA_1; 1.
PROSITE; PS01231; TRMA_2; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE002518; AAF42027.1; -. TIGR; NMB1679; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.ish-sib-ch/announce/or send an email to license@isb-sib.ch).
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Banteria; Proteobanteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transferase; Methyltransferase; tRNA processing; Complete proteome
DOMAIN 208 214 S-ADENOSYLMETHIONINE BINDING (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000051; SAM_bind.
InterPro; IPR001566; TrmA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                      243 NIEANRI 249
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                                                                                                                                                                                                                            82 NIEANRI 88
                                                                                                                                                                                                                                                                                                                                                                                             362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                             318
                                                                                                                                                                                                                                                                           conservative 0; Mismatches
                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                41309 MW;
                                                                                                                                                                                                                                                                                                                                          1.38,
                                                                                                                                                                                                                                                                                                         Score 7,
Fred. N
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                          PRT;
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                          380 AA
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35,
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CXA1_MOUSE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-96337999; PubMed-8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gorayne J.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gorayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Noverbeek R., Kirkness F.F., Weinstock K.G., Morrick T.M., Glodok A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Squyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Horodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
                                                                                                                                                                                 GJA1 OR CXN-43.
                                                                                                                                                                                                                 Gap junction alpha-1 protein (Connexin 43) (Cx43) (Gap junction 43 kDa
                                                                                                                                                                                                                                01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                         CXAI_MOUSE
P23242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
ATP-induced pore of
                                   Beyer E.C.,
                                                                                                                      Eukaryota; Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia, Eutheria; Rodentia; Schurognathi; Muridae; Murinae; Mus
                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein; Complete proteome. SEQUENCE 380 AA; 42580 MW; (3452197)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www isb-sib-ch/announce/or send an email to license@isb-sib.ch).
 "Evidence that the gap junction protein connexin-43 is the ATP-induced pore of mouse macrophages.";
                                                    MEDLINE=91217014; PubMed-1708769;
                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probom; PD011569; DUF39; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00037; fer4; 2.
Pfam; PF01837; DUF39; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGR; MJ1681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U67608; AAB99702.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Methanococcus jannaschii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002708;
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7, Conserv
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                                   Steinberg T.H.;
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                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36, Created)
36, Last sequence update)
41, Last annotation update
mouse macrophages
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 3%; Score 7;
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                                                                                                                                                                                                                                                                                                            PPT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D362219799F4796A CRC64;
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Matches
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                                                                                                                                                                                                                                                                                           SMART; SM00037; CNX; 1
                                                                                                                                                                                                                                                                                                                     Pfam; PF00029; connexin; 1. Pfam; PF03508; Connexin43; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, M61896, AAA37444.1, -. EMBL; X61576; CAA43778.1; -. FMR!; M63801, AAA53027.1, -. EMBL; X62836; CAA44640.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  second gap junction gene preferentially expressed in lung.";
J. Coll Biol 117:1299-1310(1992).
-i- FUNCTION: ONE GAP JUNCTION CONSISTS OF A CLUSTER OF CLOSELY PACKED
                                                          SEQUENCE
                                                                                        DOMAIN
                                                                                                        TRANSMEM
                                                                                                                       DUMAIN
                                                                                                                                                      DOMAIN
                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                           PROSITE; PS00407; CONNEXINS_1; PS00408; CONNEXINS_2;
                                                                                                                                                                                                                                                                                                                                                    InterPro: IPP002261; Connexin.
InterPro: IPP002261; Connexin43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAIRS OF TRANSMEMBRANE CHANNELS, THE CONNEXONS, THROUGH WHICH MATERIALS OF LOW MW DIFFUSE FROM ONE CELL TO A NEIGHBORING CELL. --
-I- FUNCTION: CONNEXIN 43 IS POSSIBLY THE ATP-INDUCED PORE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nishi M , Kumar N M , Gilula N.B.;
"Developmental regulation of gap junction gene expression during mouse embryonic development.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ruangyotavat C.P., Morgan J.L., Lo C.W.;
Submitted (SEP-1991) to the EMBL/GenBank/DDRI databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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**A PMP
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                                                                                                                                     TRANSMEM
                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                    MGD; MCI:95713; Gjal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Ricinformatics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hennemann J., Sychyna T., Lichtenberg-Frate H., Jungbluth S.,
Dahl E., Schwarz J., Nicholson B.T., Willecke K.;
"Molecular cloning and functional expression of mouse connexin40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92299686; PubMed=1318884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-CS7RL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. ALPHA-TYPE (GROUP II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Integral membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: A CONNEXON IS COMPOSED OF A HEXAMER OF CONNEXINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOUSE MACROPHAGES
                                                                                                                                                                                                                                                                                                                                                                                                                                AJUBUL, AJUBUL
                                                                                                                                                                                                                                                                                                                                                                                                                S18110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol. 146:117-130(1991).
Conservative
                                                          381 AA;
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43
75
154
175
206
227
381
            100.0%;
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                              1.3%;
Ü,
                           Score 7; DB 1;
                                                                      CYTOPLASMIC (POTENTIAL).
M -> T (IN REF. 3).
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                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                BY SIMILARITY
                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
            Pred. No.
                                                           98958A57979CEC8B CRC64;
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91337077; PubMed=1651718; Tohn S A , Revel J.-P.; "Connexon integrity is maintained by non-covalent bonds: intramplemular disulfide bonds link the extracellular demains connexin-43.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-85207650; FubMed+2987225;
Nicholson B.J., Gros D.B., Kent S B H , Hood T.E., Revel J -p
"The Mr 28,000 gap junction proteins from rat heart and liver
                                                                                                                                                                                                                                                         MEDLINE-92167270; FubMed=1371548;
Yeager M., Gilula N.B.;
"Membrane topology and quaternary structure of cardiac gap junction
ion channels.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dupont E., el Aoumari A., Fromaget C., Briand J.-C., Gros "Affinity purification of a rat-brain junctional profein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=91348048; PubMed=1652440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             different but related."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91241281; PubMed=1852114;
Lang L M , Beyer E.C , Schwart? A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Connexin43: a protein from rat heart homologous to a gap junction protein from liver ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINF=880∺7<45; PupMed=2826492;
Beyer E C , Paul D L , Goodenough
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1988 (Pel. 09, Last sequence update)
16-OCT-2001 (Pel. 40, Last annotation update)
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                                 -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- PTM: THERE IS AT LEAST ONE INTRAMOLECULAR DISHLETOE FOND
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochem. Biophys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFIDE HONDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lang L M. Heyer E.C., Schwart? A L., Gitlin T. P.; Molecular cloning of a rat uterine gap junction protein and analysis of gene expression during gestation."; Am. J. Physiol. 260:E787-E793(1991).
-!- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. ALPHA-TYPE (GROUP II)
                                                                                                                                                                                                                                                                                                                                                                                              IOPOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eur. J. Biochem. 200:263-270(1991)
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                                                                                         MATERIALS OF LOW MW DIFFUSE FROM ONE CELL TO A NEIGHBOFING CELL. SUBBUILT: A CONNEXON IS COMPOSED OF A HEXAMER OF CONNEXINS.
                                                                                                                                                            AND BIOL 223:929-948(1992)
FUNCTION: ONE GAP JUNCTION CONSISTS OF A CLUSTER OF CLOSELY PACKED PAIRS OF TRANSMEMBRANE CHANNELS. THE CONNEXONS. THEOUGH WHICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 VNVEMHL 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               υθνωδ9; υθνυ70; υθκγυ6;
16·007-2901 (Rel. 40, Created)
16-007-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Fokaryota, Metoroa, Chordati, Crantata, Vertebrata; Batch
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00029; connexin; 1.
Pfam; PF03508; connexin43; 1.
PFINTS. PF00206; CONNEXIN
SMART; SM00037; CNX; 1.
                     -1- SUBCELLULAR LUCATION: Nuclear (Probable).
-1- SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.
-1- SIMILARITY: CONTAINS 2 LIM IMMAINS THE L
                                                                                                                       Fellous M., Berkovitz G.D., McElreavey K.;
"Absence of mutations involving the LIM homeobox domain gene LHX9 in 46,XY gonadal agenesis and dysgenesis.";
olin Endocrinol Metab 86.2465.2469(2001).
                                                                                                                                                                                                                                MEDLINE-21291005, FubMed-11397841,
Ottolenghi C., Moreira-Filho C., N
                                                                                                                                                                                                                                                                                   TISSUE-Testis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LHX9_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIP: SUUS32: SUUS32
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                                                                                                 -!- FUNCTION: INVOLVED IN GONADAL DEVELOPMENT (BY
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIM/homeobox protein Lhx9.
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Interpro: IPR002261; Connexin43.
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A -> T (IN REF. 2).
V -> I (IN REF. 3).
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Best Local
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30-MAY-2000 (Rel 4, Created)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD000010; Homeobox; 1
ProDom; PD000094; LIM; 2.
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EMBL; AJ277916; CAF98128.1;
EMBL; AJ277917; CAB98128.1;
EMBL; AJ277918; CAB98128.1;
EMBL; AJ277919; CAB98128.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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Pfam; PF00412; LIM; 2
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Genew; HGNC:14222; LHX9
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or send an email to licensedisb sib.ch).
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                                                                                                  STRAIN-NIH Swiss;
                                                                                                                                                                                                                                                                                                                           Retaux S., Rogard M., Bach I., Failli V., Besson M.J. "Lhx9: a novel LIM-homeodomain gene expressed in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
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                                                 MEDLINE=99264291; PubMed=10330499;
                                                                                                                                              SEQUENCE OF 11-388 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-99098964; PubMed-9880598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-C57BL/6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-300 FROM N.A.
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                                                                                                                                                                                                                                       Neurosci. 19:783-793(1999).
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AJ296272; CAC33174.1;
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258
Porter F.D , Pitts A .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114
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317
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Kumar M., Agulnick A., Wassif C.
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Query Match

Rest Local Similarity
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EMBL: AF113518;
EMBL: AJ243851;
EMBL: AJ243852;
EMBL: AJ243854;
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                    Produm, Promouto; Homosbox; 1. Prodom; PD000094; LIM; 2. SMAPT; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                         Pfam; PF00046; homeobox; 1. Pfam; PF00412; LIM; 2.
                                                                                                                                                                                                                                                                                                TRANSFAC: T04192: -.
TRANSFAC: T04195: -.
MGD: MGI: H16771: lhxq
InterPro: IPR001356: Homeobox.
InterPro: IPR001781: LIM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Failli V., Rogard M., Mattel M.-G., Vernier P., Retaux S.; "Lhx9 and Lhx9alpha LIM-homeodomain factors: genomic structure, expression patterns, chromosomal localization, and phylogenetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C5781/6, TISSUE-Brain;
MEDLINE=20221375; PubMcd-10756098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING STRAIN-C5781/6, TISSUE-Brain;
                                                                                                                                                                                                    PPOSITE; PSOOO27; HOMEOBOX_1; 1. PROSITE; PSSOO71; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to licensewisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Furopean Bioinformatics Institute. There are no restrictions on its the produced through a sits content is in no way use by non-profit institutions as long as its content is in no way
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Meth fev 81 193-198(1999).
                                                                                                                                             DOMAIN
                                                                                                                                                       Metal-binding; Zine;
                                                                                                                                                                 PROSITE; PS50023; LIM_DOMAIN_2; 2.
Homeobox; DNA-binding; Nuclear protein; Repeat; LIM domain;
                                                                                                                                                                                         PROSITE; PS00478; I.IM_DOMAIN_1;
                                                                                                                                                                                                                             SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AJ243855;
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                                                                                                                                 DOMAIN
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AJ243852;
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                                   388 AA;
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153
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AAD22008.1;
CAB59907.1;
CAB59908.1;
                                                                                                                                                                                                                            LIM; 2
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S -> F (IN REF. 2).
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TPPGTATTLTDLTNPTVTVVTTVISMNUSHEMSPSOTTLT
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PCY2_HUMAN
ID PCY2_HIMAN
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AC Q99447
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16-OCT-2001 (Pel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Ethanolamine-phosphate cytidylyltransferase (EC 2 7 7 14)
(Phosphorylethanolamine transferase) (CTP:phosphoethanolamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as iong as its content is in mo modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nakashima A., Hosaka K., Nikawa J.;
"Cloning of a human cDNA for CIP-phosphoethanolamine
cytidylyltransferase by complementation in vivo of a yeast mutant.",
J. Biol. Chem. 272:3567-9572(1997).
                                                                                                                                                                                                                                                                                                             InterPro; IPR004821; Cyt_tran_rel.
InterPro; IPR004820; Cytidylytransf.
Pfam; PF01467; Cytidylytransf; 2.
TIGPPAMs: TIGR00125; Cyt_tran_rel; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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Mammalla, Futheria; Primates,
                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                            Transferase, Nucleotidyltransferase; Phospholipid biosynthesis DOMAIN 20 194 CATALYTIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                           MIM; 602679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL: BCOOO351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to licensemisb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entitles requires a license agreement (See http://www.isb-sib ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE CYTIDYLYLTPANSFERASE FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDP-ethanolamine.
PATHWAY: PHOSPHOLIPID BIOSYNTHESIS; CDP-ETHANOLAMINE SYNTHESIS;
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                                                    151 TLETLDK 157
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BC000351: AAH0035111; -
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                                                                                                                                                                                                                                389 AA;
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Catarrhini, Hominidae
                                                                                                                                       Pred. No.
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Subtilist: BG10102; argJ.
InterPro; IPR002813; ArgJ.
Pfam: PF01960; ArgJ; 1.
Probom, PD094133, ArgJ, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arginine biosynthesis bifunctional protein argJ [Includes: GiutaMate N-acetyltransferase (EC 2.3.1.35) (Ornithine acetyltransferase) (Ornithine transacetylase) (OATASE); Amino-acid acetyltransferase
                                                                                                                                                  TIGRPAMS; TIGRO3120; ArgJ; 1.
AL4Juliu blusynthesis; Transforase; Acyltransferase;
Multifurctional charme; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (Some http://www.ish-sib ch/announce.or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -:- CATALYTIC ACTIVITY: N(2)-acetyl-L-ornithine + L-ylutamate = L-ornithine + N-acetyl-L-glutamate.
-:- CATALYTIC ACTIVITY: Acetyl-CoA + L-glutamate = CoA + N-acetyl-L-
                                                                                                                                       SECHENCE
                                                                                                                                                                                                                                                                                                EMBL; 299109; CAB12961.1; -. EMBL; 299110; CAB12977.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glutamate.
-i- pathway- first and firth steps in Apgining Biosynthesis-
-i- subunit: Homodimer (BY_SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Sequence and analysis of the citrulline biosynthetic operon {\tt argC-F} from {\tt Bacilius} subcilis:";
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15-JUN-2002 (Pel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P36843;
01-JUN-1994

    -i- SUBCELLULAR LOCATION: Cytoplasmic (Probable).

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Midrobiology 143.3305-3308(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        degrees) in Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Medina N , Vannier F , Rowhe B . Autret 3 , Levine A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98015415; PubMed=9353931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-80 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Midrobiology 148.1023-1025(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-94197711; PubMed-8015667;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
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Copyright (c) 1993 - 2003 Compug
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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   US-09-385-259-3
US-09-645-370-3
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US-08-447-314-12
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US-08-445-461-10
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US-08-445-4010-10
US-08-170-558-10
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US-08-170-558-11
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US-08-170-558-11
US-08-170-558-11
US-08-170-952-756
US-08-447-314-10
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US-09-90-90-793-8
US-08-375-709-13
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Sequence 3, Appli
Sequence 12, Appl
Sequence 12, Appl
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Sequence 12, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 6, Appli
Sequence 10, Appli
Sequence 16, Appli
Sequence 1756, Appli
Sequence 1756, Appli
Sequence 13, Appli
Sequence 28, Appli
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SEQ ID NO 3

SOFTWARE: PatentIn Ver. 2.0

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Sequence 474, App	Sequence 3, Appli		Sequence 44, Appl	Sequence 49, Appl	Sequence 7, Appli	Sequence 7, Appli	Sequence 382, App	Sequence 14, Appl	Sequence 21, Appl	Sequence 18, Appl	Sequence 18, Appl	Sequence 22, Appl	Sequence 21, Appl	Sequence 20, Appl	Sequence 6, Appli	Sequence 89, Appl	Sequence 28, Appl

ALIGNMENTS

US-09-385-259-3

Sequence 3, Application US/09385259 Patent No. 6201114

GENERAL INFORMATION:
APPLICANT: Aguirre, Gustavo D.
APPLICANT: Aguirre, Gustavo D.
APPLICANT: Acland, Gregory M.
APPLICANT: Ray, Kunal
TITLE of INVENTION: IDENTIFICATION OF CONSENITAL STATIONARY NIGHT BLINDNESS
TITLE OF INVENTION. IN DOGS
FILE REPERENCE. 19603/2481
CURRENT APPLICATION NUMBER: US/09/385,259
CURRENT APPLICATION NUMBER: MS/09/385,259
EARLIER APPLICATION NUMBER: MS/09/385,259
EARLIER FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 8
NUMBER OF SEQ ID NOS: 8

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                                                                                                                                                                                                                                                                  ; Sequence 3, Application US/09645370 ; Patent No. 6428958 ; GENERAL INFORMATION:
                                                        APPLICANT: AQUITE, GUSTAVO D.
APPLICANT: Acland, Gregory M.
APPLICANT: Ray, Kunal
TITLE OF INVENTION: IDENTIFICATION OF CONSENTTAL STATIONARY NIGHT BLINDNESS
TITLE OF INVENTION: IN DOGS
FILE REFERENCE. 19603/2481
CURRENT APPLICATION UMMBER: US/09/645,370
CURRENT APPLICATION NUMBER: 09/385,259
PRIOR APPLICATION NUMBER: 09/385,259
PRIOR APPLICATION NUMBER: 09/385,259
PRIOR FILING DATE: 1999-08-30
PRIOR FILING DATE: 1999-08-30
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PRIOR AFFLICATION NUMBER: 60/103,219 PRIOR FILING DATE: 1998-10-06 NUMBER OF SEQ ID NOS. 8
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TYPE: PRT
OKGANISM: Canis familiaris
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Local Similarity 100.0%; F
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                                                                 Query Match 1.5%: Score 8; DB | Hest Local Similarity 100.0%: Pred. No. 13; Matches 8; Conservative 0; Mismatches
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                                                                                                                                                                                                    TELEPHONE: 415/225-1896
TELEFAX: 416/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PKT
ORGANISM: Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: patin (Geneatech)
CURRENT APPLICATION DATA:
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APPLICANT: Mark, Melanie R.
APPLICANT: Scadden, David T.
APPLICANT: Baker, Kevin P.
APPLICANT: Baron, Will F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Protein Tyrosine Kinases NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 415/225-1896
                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER - 08/15
FILING DATE: 23-NOV-1993
AUTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER- 08/170558
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANDRESSEE: Generitech, Inc.
STEPRET: 460 Point San Bruno Blyd
CITY: South San Francisco
STATE: California
                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 22-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                              NAME: Hasak, Janet E. REGISTRATION NUMBER: 28,616
                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                   REFERENCE/DOOKET NUMBER: 85402
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210 DGLALLHS 217
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                                  52 DGLALLHS 59
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100.0%; Pred. No.
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US-08-170-558-12
                                                                                                                                                                                                                                                                                      RESULT 5
                                                                                                                                                                                         Sequence 12, Application HS/08447314
Patent No. 6087144
GENERAL INFORMATION:
APPLICANT: Scadden, David T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/08170558 Patrent No. 6001621
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Matches 8, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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AFFLICATION NUMBER: 08/157563
AFFLICATION BATE: 23.NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
PEGISTRATION NUMBER: 28,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Godowski, rau. ...
APPLICANT: Mark, Melanie R.
APPLICANT: Scadden, David T.
APPLICANT: Bakar: Keyin P.
                                                                                                                                                         APPLICANT: Baker, Kevin F
APPLICANT: Baron, Will F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 85
IELECOMMUNICALION INFORMATION:
TELEPHONE: 415/255-1896
TELEPAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IHM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genertech) CURRENT APPLICATION DATA:
                                                                                                    NUMBER OF SEQUENCES: 3
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                                                                                                                                          TITLE OF INVENTION: Protein Tyrosine Kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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                                                  STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
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CITY: South San Francisco
STATE: California
                COUNTRY:
                                     STATE:
                                                                                       ADDRESSEE:
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TELEX: 910/371-7168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER US,08/170,558 FILING DATE: 20-DEC-1993
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94080
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23-NOV-1993
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MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Generatech)
CUPPENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/255-1896
TELEFAX: 415/952-9881
                                                       APPLICATION NUMBER: US/08/445
FILING DATE: 22:MAY:1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/170558
FILING DATE: 20-DEC-1993
                                                                                                                                                                   SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                       COMPUTER READARIE FORM.
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Baker, Kevin P. APPLICANT: Baron, Will F. TITLE OF INVENTION: Protein
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APPLICANT: Mark, Melanie R.
APPLICANT: Scadden, David T.
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APPLICATION NUMBER: 08/1:
FILING DATE: 23-NOV-1993
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 08/170558
FILING DATE: 20-DEC-1993
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                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
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les 8; Conserv
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amino acid
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UMBER: 08/157563
23-NOV-1993
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L00.0%; Pred. No 13;
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; Patent No. 5679772
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Best Local :
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TELEPHONE: 415/225-1896
TELEPAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 12:
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                                                                                                                                                                                                                                  TELEPHONE: (212) 688-9200 TELEFAX: (212) 838-3884 THEORMATION FOR SEC ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: B vik, Claes Olof; Eriksson, Ulf; Peterson, Per A. illie OF INVENTION: Isolated Protein Receptors, Antibodies Which Hills OF INVENTION: bind Thereto, Nucleic Acid Sequence Coding
                                                                                                                                                                                              SEQUENCE CHARACTERISTICS.
LENGTH: 533 amino acid
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CURRENT APPLICATION DATA:
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LENGTH: 388 amino acids
TYPE: amino acid
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NAME: Kohli, Vineet
PEGISTRATION NUMBER: 37,003
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MEDIUM TYPE: Diskett
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                                                                                                                                                                               LENGTH: 533 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/488,305A FILING DATE: 7-JUNE-1995 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PS/
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York City
STATE: New York
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Local Similarity 100.0%; Pred. No. 13,
Les 8, Conservative 0, Mismatches
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109 PDPCKNIF 116
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                                 99 PDPCKNIF 106
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                                         : Sequence 6, Application US/08456647B
: Patent No. 5811516
                                                                              US-08-456-647B-6
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US-09-385-259 2
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GENERAL INFORMATION:
APPLICANT: Lemke Ph.D. et al., Greg E.
                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                Best Local Similarity 100.0%;
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CORRENT FILLING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 09/385,259
PRIOR FILLING DATE: 1999-08-30
PRIOR PILLING DATE: 1999-08-30
PRIOR PILLING DATE: 1998-10-06
PRIOR PILLING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/385,259
CURRENT FILING DATE: 1999-08-30
EARLIER APPLICATION NUMBER: 60/103,219
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NUMBER OF SEQ ID NOS. 8
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APPLICANT: Acland, Gregory M.
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                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0
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ORGANISM: Canis familiaris
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                                                                                                                                                                                                                                                                                                                                                                LENGTH: 533
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                Length 533;
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                                                                                                                                                                                                                               Indels
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US-08-237-401A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local Similarity 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/237,401
FILING DATE: 02-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER- US 07/8%4,4%6
FILING DATE: 15-MAY-1992
AITO-MNEY-JAGENT INF-OWN-TICNI
NAME: Wetherell Ph.D., John R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: 07251/007002
TELECOMMUNICATION INF-ORMATION:
TELECOMMUNICATION 1NF-ORMATION:
TELECOMMUNICATION 1NF-ORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (619) 678-5099 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DUS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                     APPLICANT: Lemke Ph.D. et al., Greg E.
TITLE OF INVENTION: PROTEIN-TYROSINE KINASE GENES
NUMBER OF SEQUENCES: 54
CORKESFONDENCE ADDRESS:
PRIOR APPLICATION DATA:
                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 530
CRASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/237,401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: PROTEIN-TYPOSINE KINASE GENES NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
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                  APPLICATION NUMBER: FILING DATE: 02-MAN CLASSIFICATION: 435
                                                                                                                                                                                                                                CITY: La Jolla
STATE: CA
                                                                                                                                                                                              ZIP:
                                                                                                                                                                                                                                                                     ADDRESSEE: Fish & Richardson P.C. STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U
ZIP: 92037
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                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IRM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                  02-MAY-1994
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                                                      US/08/237,401A
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RESULT 12
US-08-445-640-10
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                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/445,6
FILING DATE: 2-WAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA: 08/170558
FILING DATE: 20-OPEC-1993
PRIOR APPLICATION DATA:
APPLICATION UMBER: 08/157563
FILING FAIE: 24-N-V-1993
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEPAX: (619) 678-5099
INFORMATION FOR SEQ ID NO. 6.
SEQUENCE CHARACTERISTICS:
                                                                         INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-POS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION: NAME: Hasak, Janet E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION. Protein Tyrosine Kinases NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Godowski, Paul |
APPLICANT: Mark, Melanie P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Haile Ph.D., Lisa A.
                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity hes 8; Conserv
                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
LENGTH: 880 amino acids
TYPE: amino acid
TOPOLOGY: linear
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T: Baron, Will F.
INVENTION. Proteir
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15-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.5%; Score 8; DB 2;
100.0%; Pred No 27;
ative 0; Mismatches
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                                                                                                                                                                                   28,616
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RESULT 14
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Best Local :
                                                                                                             Matches
                                                                                                                              Query Match
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                                                                                                                                                                                                                                                            INFORMATION FOR SEC ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Baker, Kevin P.
APPLICANT: Baron, Will F.
TITLE OF INVENTION: Protein Tyrosine Kinases
NUMBER OF SEQUENCES: 35
CORPESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 85
TELECOMMUNICATION INFORMATION: 415/225-1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Godowski, Paul J.
APPLICANT: Mark, Melanie R.
APPLICANT: Scadden, David T.
                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 880 amino acid
                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 23-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA: APPLICATION NUMBER:
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                                                                                            1.5%; Score 8;
local Similarity | 100 0%; Pred No.
hos 4; Conscrivativo 0: Michael
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CITY: South San Francisco
                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                             TYPE:
                                                                                                                                                                                                                                                                                         TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
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                                              240 DGLALLHE 247
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                                                                              52 DGLALLHS 59
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Similarity 100.0%; Pred. No. 27,
8; Conservative 0; Mismatches
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                                                                                                             Mismatches
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o. 27;
                                                                                                                                            DB 3;
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                                                                                                                                          Length 880;
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                                                                                                            Gaps
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; sequence 10, Application US/08447314 ; Patent No. 6087144

GENERAL INFORMATION:

APPLICANT: Scadden, David T. APPLICANT: Baker, Kevin P.

US-08-447-314-10

APPLICANT:

Baron, Will F.

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US-08-445-461-10
: Sequence 10, Application US/08445461
; Patent No. 6096527
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US-08-447-314-10
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                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 10:
                                                          COMPUTER READABLE FORM: MEDIUM TYPE: 5 25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                               TITLE OF INVENTION: Protein Tyrosine Kinases NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                           APPLICANT: Godowski, Paul J.
APPLICANT: Mark, Melanie R.
APPLICANT: Scadden, David T.
APPLICANT: Baker, Kevin P.
APPLICANT: Baron, Will F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 85
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: ITMM PC compatible
OPERATING SYSTEM: PC-DUS/MS-DUS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 880 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/157563
FILING DATE: 23-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/170558
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Protein Tyrosine Kinases NUMHER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-SOFTWARE: patin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
STREET: 46
                                                                                                                             COUNTRY:
                                                                                                                                                     STATE:
                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/447,314 FILING DATE: 22-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: South San Francisco
STATE: California
                                                                                                          ZIP: 94080
                                                                                                                                                                                                               ADDRESSEE:
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TELEX: 910/371-7168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Hasak, Janet E. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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South San Francisco
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Baron, Will F.
                                                                                                                             USA
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Job time : 28 secs
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Best Local Similarity 100.0%;
Matches 8; Conservative (
                                                                                                                                                                                                                                                                                           INFURMATION FOR SEC ID NO:
                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 880 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 85-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEPFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,461
FILLING DATE: 22-MAY-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 23-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA: APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                    TELEFAX: 415/752-70
TELEX: 910/371-7168
                                                                                                                                                                                                                                                                                                                                                                                              NAME: Hasak, Janet REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/1 FILING DATE: 20-DEC-1993
                                                                     240 DGLALLHS 247
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23-NOV-1993
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1ve 0; Mismatches
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/cgn2_6/ptodata/1/pubpaa/USOF_PUB-PUB_Pep.*
/cgn2_6/ptodata/1/pubpaa/USOF_PUB-TMH_PEP.*
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•	Sequence 149, App	Sequence 148, App	Sequence 118, App		Sequence 621, App	Ξ.	Sequence 1, Appli	Sequence 6, Appli	Sequence 2, Appli	Sequence 37, Appl	Sequence 5, Appli	٠,	Sequence 5, Appli	Sequence 3, Appli	7,		Sequence 4, Appli	Sequence 1, Appli	Description

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-	_	~				Sequence 606, App			Sequence 49. Appl	Sequence 127, App	Sequence 271, App	5	Sequence 10, Appl	Sequence 8239, Ap	Sequence 192, App	Sequence 9, Appli	Sequence 3239, Ap	S-40+000 7990, Ap	Sequence 8, Appli	Sequence 2. Appli	Sequence 5295, Ap	Soguence 4922, Ap	Sequence ind, App	Sequence 64, Appl	Sequence 60, Appl

ALIGNMENT

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; TYPE: PRT
; ORGANISM: CHICKEN
US-10-053-192-1
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Fublication No. US/6030087336A1
; GENERAL INFORMATION:
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SOFTWARE: PatentIn Ver. 2.1
SEQ 10 NO 1
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Hest Local Similarity 100.0%; Pred. No. 0;
Matches 526; Conscivative O. Mismatches O. Indols O: Caps
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION BETA, RETA-CAROTENE 15,15° (BLOXYGENASES, NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES CODING THEREFOR AND THEIR USE
FILE PRIERENCE: R. B-CAROTENE 15,15°-DTOXYGENASES.
CURPENT APPLICATION NUMBER: US/10,763,102
CURPENT FILLING DATE: 2002-01-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 103382.0 PRIOR FILING DATE: 1999-02-22
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121 TONCOLINIMKTGOPYVATSETNEJPKIDPGTLETLDKVDYSKYVAVNLATSHPHYDSAGN
                                                     121 TONGLINIMKTGHTYYATSETNETEKLDPQTLETLDKVDYSKYVAVNLATSHPHYDSAGN 180
                                                                                                      61 JEKNYJEVYYESKYLESIG YN'NI FANE IVVSEE JIMAYEGG'ENIFAFAFYY SHEJPEF 120
61 JEKNYJEVYYESKYLESIG YN'NI FANE IVVSEE JIMAYEGG'ENIFAKAF SYLSHTLEFEF 120
                                                                                                                                                                                                                                                         1 METTENENKEEHPEPTKAEVQGQLPTWLQGVILENGEGMHTIGETKYNHWELGLALLHSE 60
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WYSS, Markus
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WIPTZ, Gabriele M
WOGGON, Wulf-Dietrich
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APPLICANT: BRUGGER, Roland
APPLICANT: FRIEDLEIN, Arno M
APPLICANT: WIRTZ, Gabriele M
APPLICANT: WOGGON, Wolf-Dietrich
APPLICANT: WYSS, Adrian
APPLICANT: WYSS, Markus
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Publication No. US20030087336A1
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LENGTH: 506
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CURRENT FILING DATE: 2002-01-15
PRIOP APPLICATION NUMBER: 103382.0
PRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: BETA, BETA-CAROTENE 15,15'-DIOXYGENASES, NUCLEIC ACID TITLE OF INVENTION: SEQUENCES CODING THEREFOR AND THEIR USE FILE REFERENCE: H,H-CAROTENE 15,15'-DIOXYGENASES,...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: CHICKEN
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                                              190 DKGFTKYVLFKIPSSVPEKEKKKSCFKHLEVVCSIPSRSLLQPSYYHSFGIIENYIVFIE 249
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                    181 DKGRTKYVLFKIPSSVPEKEKKKSCFKHLEVVCSIPSRSLLQPSYYHSFGITENYIVFIE 240
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                                                                                                                                                                                                                                                                                                                                                                             96.2%; Score 506; DB 9, Length 506; Similarity 100.0%; Pred. No. 0; Ob; Conservative 0; Mismatches 0; Indels
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                                                                                                           KTGDDYYATSETNFIRKIDPQTLETLDKVDYSKYVAVNLATSHPHYDSAGNILNMGTSIV 180
                                                                                                                                    KTGDDYYATSETNFIRKIDPQTLETLDKVDYSKYVAVNLATSHPHYDSAGNILNMGTSIV 189
                                                                                                                                                                                                 RSKYLRSDTYNCNIEANRIVVSEFGTMAYPDPCKNIFAKAFSYLSHTIPEFTDNCLINIM 120
                                                                                                                                                                                                                                           RSKYLRSDTYNCNIEANRIVVSEFGTMAYPDPCKNIFAKAFSYLSHTIPEFTDNCLINIM 129
                                                                                                                                                                                                                                                                                       EEHPEPIKAEVQGQLPTWLQGVLLRNGPGMHTIGDTKYNHWFD3LALLHSFTFKNGEVYY 60
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CURPENT APPLICATION NUMBER
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RESULT 4
US-10-053-192-7
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                                                                                    APPLICANT: HACHMANN, Heinrich
APPLICANT: BRUGGER, Keland
APPLICANT: FRIEDLEIN, Arno M
APPLICANT: WIRTZ, Gabriele M
APPLICANT: WOSGON, Wolf-Dietrich
APPLICANT: WYSS, Adrian
APPLICANT: WYSS, Markus
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Ouery Match
Best Local Similarity 100.0%; Pred. No. 3.6e-10;
Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/10053192
Publication No. US/003008/336Al
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CURPENT APPLICATION NUMBER- US/10/053,192
CURRENT FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER- 103382 0
PRIOR APPLICATION NUMBER- 103382 0
FITLE OF INVENTION: BETA, RETA CARCTENE 15,15' DICKYCHASES, MUCLEIC ACTU
TITLE OF INVENTION: SEQUENCES CODING THEREFOR AND THEIR USE
FILE REFERENCE: B,B-CARCTENE 15,15'-DICKYCHNASES,...
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APPLICANT: BRUGGER, Heiand
APPLICANT: FRIEDLEIN, Arno M
APPLICANT: WIRTZ, Gabriele M
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WYSS, Markus
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RESULT 6
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Best Local Similarity
Thes 8, Conserve
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Patent No. US20020137168A1
GENERAL INFORMATION:
AFFLICANT: CROSIER, PHILIP S.
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APPLICANT: WYSS, Markus
TITLE OF INVENTION: BETA, BETA-CAROTENE 15,15'-DIOXYGENASES, NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES CODING THEREFOR AND THEIR USE
FILE REFERENCE: B,B-CAROTENE 15,15'-DIOXYGENASES,...
CURRENT APPLICATION NUMBER: US/10/053,192
CURPENT FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER-103382 0
PRIOR FILING DATE: 1994-02-22
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APPLICANT: BRUGGER, Roland
APPLICANT: FRIEDLEIN, Arno M
APPLICANT: WIRTZ, Gabriele M
APPLICANT: WOGGON, Wolf-Dietz
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PPTOR APPLICATION NUMBER: 103382.0
PRIOR FILING DATE: 1999-02-22
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ORGANISM: CHICKEN
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                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C
                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                           18 AEVQGQLP 25
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STATE: VIRGINIA
COUNTRY: II S A
ZIF: 22201-4714
                                                     CITY: ARLINGTON
                                                                        STREET: 1100 NORTH GLERF POAD
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WOGGON, Wolf-Dietrich
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100.0%; Pred No 3 he-1
vative 0, Mismatches
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100.0%; Pred. No. 4e+0
ative 0; Mismatches
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: SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-985-675-5
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Bost Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: GOGOWSAL, APPLICANT: Mark, Melanie R. APPLICANT: Scadden, David T. APPLICANT: Scadden, David T.
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb:
COMPUTER: IBM CC compatible
OPERATING SYSTEM: PC-1-05/MS-FOS
SOFTWARE: patin (Genentech)
CURFENT APPLICATION DATA:
                            ATTOPNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,
                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
REFERENCE/DOCKET NUMBER: 85
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Protein Tyrosine Kinases
                                                                                        FILING DATE:
                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                  STREET: 460 Point San Bruno Blvd CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity es 8; Conserv
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ATTOPNEY/AGENT INFORMATION:
NAME: MIICHARD, LEGNARD C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERFNCE/DOCKET NUMBER: 175-19 TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE, Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (703) 816-4100
TELEFAX: (703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 29,009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/505,241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                   California
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Baron, Will F.
                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                             08/170,558
                                                                                                                                                                                  US/09/223,490
                                  28,616
                                                                                                                                                                                                                                                                          360 Kb floppy disk
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APPLICANT: HACHMANN, Heinrich
APPLICANT: FRUGGFR, Poland
APPLICANT: FREDLEIN, Arno M
APPLICANT: WIKTZ, Gabriele M
APPLICANT: WOGGON, Wolf-Dietrich
APPLICANT: WYSS, Adrian
APPLICANT: WYSS, Markus
                                                                                                                                                                                                                                                                             US-09-928-457-37
: Sequence 37, Application US/09928457
: Patent No. US20020144603A1
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Publication No. US20
GENERAL INFORMATION:
APPLICANT: BACHMANN
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                                                                                                                                                                                                                                                                                                                                                  RESULT 9
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SEQ ID NO 5
LENGTH: 529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: BETA, HETA-CAROTENE 15.15'-DIOXYGENASES, NUCLEIC ACID TITLE OF INVENTION - SEQUENCES CODING THEPEORE AND THEIR USE FILE REFERENCE 'R, B-CAROTENE 15.15'-DIOXYGENASES,... CURRENT APPLICATION NUMBER, US/10/053,192
CURRENT FILING DATE: 2002-01-15
                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 103382.0 PRIOR FILING DATE: 1999-02-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 10
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TELEX: 910/371-7168
INFORMATION FOR SEO ID NO: 12.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                          APPLICANT:
TITLE OF INVENTION: I
TITLE OF INVENTION: I
TITLE OF INVENTION: I
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: BOVINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patenth Release #1.0, Version #1.30 (OEB)
CURRENT APPLICATION DATA:
                                                                                                                                            COMPUTER READABLE FORM:
      FILING DATE:
                    APPLICATION NUMBER:
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JMHFP: US/09/928,457
2001-08-14
                                                                                                                                                               DNA, specific proteins and peptides of the Neisseria method for obtaining them and their biological application.
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US-09-985-675-2
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                 Query Match 1 5%:
Best Local Similarity 100.0%;
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 Matches
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                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 2:
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APPLICATION NUMBER:
FILING DATE: 199-12-
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nes 8; Conserv
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TOPOLOGY: lir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTEK: IBM PC compatible

OPERALING SYSTEM: PC-TO-SyMS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
                                                                                        TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/505,241 FILING DATE: 16-AUG-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: CROSIER, PHILIP S. CROSIER, KATHRYN E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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FILING DATE: 05-No. US20020147168A1-2001
CLASSIFICATION: <Unknown>
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                                                                                                                                                    TYPE: AMINO ACID
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TELEFAX: (703) 816-4100
                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 175-19
                                                                                                                                                                                                                                                                                                                     NAME: MITCHARD, LEONARD C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
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Conservative
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100.0%; Pred. No
                   ] 5%; Score 8; DB 10;
100.0%; Pred. No. 57;
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0; Mismatches
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                 Pred. No.
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                                     Length 850;
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US-09-985 675-1
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US-09-158-722-6
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                                                                                                                               Sequence 1, Application US/09985675
Patent No. US20020137168A1
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHAPACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Wetherell Ph.D., John R.

PEGISTRATION NIMHER: 31,678

PEFERENCE/TWOKET NUMER: 01251/007902

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/884,486
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/456,647
FILING DATE: 02-IUN-1995
APPLICATION NUMBER: US 08/237,401
FILING DATE: 02 MAY-1994
PRICH APPLICATION FAIA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: PROTEIN-TYPOSINE KINASE GENES
NUMBER OF SEQUENCES: 54
                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.0%; tes 8; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Pelease #1 0, Version #1 25
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CITY: La Jolla
STATE: CA
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COPPESPONICAVE ALGERSS:
ADDRESSEE: NIXON & VANDERHYE P.C
                                                                                                         APPLICANT: CROSIER, PHILIP S
                                       NUMBER OF SEQUENCES: 16
                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                234 DGLALLHS 241
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4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        874 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                            CROSIER,
                                                                                                                                                                                                                                                                                                                                                                          1.5%,
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                                                      DEVELOPMENTAL TYPOSINE KINASES AND THEIR LIGANDS
                                                                                            KATHRYN E
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                                                                                                                                                                                                                                                                                                                                                       Score 8,
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TOPOLOGY: LINEAR

MOLECULE TYPE: PROTEIN
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-985-675-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 10, Application US/U9223490; Patent No. US20020147325A1; GENERAL INFORMATION:
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US-09-223-490-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                               MEDIUM TYPE: 7.25 linch, 360 Kb. 1
COMPUTER: HEM PC compactible
JPERALING SYSIEM: PC-1905/MS-1/OS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                       COMPUTER READARLE FORM:
                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Protein Tyrosine Kinases NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Baker, Kevin P. APPLICANT: Baron, Will F
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Mark, Melanie R. APPLICANT: Scadden, David T
                                                                                                                                                                                                                                                                                                                                                   CHRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT
                                      FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                         CITY: South San Francisco
                                                                                                                                                                                                                                                                                                          ADDRESSEE: Genentech, Inc. STREET: 460 Point San Bruno Blvd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100.0%;
les 8; Conservative (
                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 175-19 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURPENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 DGLALLHS 241
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OPERATING SYSTEM: PC-1058/MS-TOS
SOFTWAPE: Patentin Pelease #1.0, Version #1 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1100 NORTH GLERE POAD CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/985,675
FILING DATE: 05-NO. US2UULU13/168A1-2UU1
CLASSIFICATION: /Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: MITCHARD, LEONARD C
PEGISTRATION NUMBER 29,00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AFFLICATION NUMBER: 08 08/505,241 FILING DATE: 16-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                   California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
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                                                                                                                                                                                                                                                  USA
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  69/1/0/558
                                                                                US/09/223,490
                                                                                                                                                                                 360 Kb floppy disk

    Mismatches

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Pred. No.
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ATTORNEY/AGENT INFORMATION:

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                                                                                                                                                                                                                                                                                                                                                         Sequence 34560, Application US/09864761 Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 621
LENGTH: 23
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                            PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                        APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROFES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/809,391 CURRENT FILING DATE: 2001-03-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ruben et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P2
PRIOR APPLICATION NUMBER: US 09/632,366 PRIOR FILING DATE: 2000-08-03 PRIOR APPLICATION NUMBER: GB 24263.6
                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/864,761 CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                              APPLICANT: Penn, Sharron G
APPLICANT: Rank, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 10:
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hes 8; Conservative
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hasak, Janet E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (; 415/952-9881
910/371-7168
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100.0%; Pred. No.
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Search completed: July 15, 2003, 09:50:21

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Query Match
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LENGTH: 32
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FRIOP FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-06-30
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PRIOR APPLICATION NUMBER: PCT/US01/00670
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PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                    164 VAVNLAT 170
                                                                                                                                                                              INFORMATION:
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23 VAVNLAT 29
                                                                             Conservative
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                                                                                                                                                                                                                                                                                EXPRESSED
EXPRESSED
                                                                                                                                                                            EXPRESSED IN HELA, SIGNAL 4.8
EXPRESSED IN LUNG, SIGNAL 4.8
FXPPESSED IN HRITO, SIGNAL 4.1
EXPRESSED IN HONE MARROW, SIGNAL - 5.1
EST_HUMAN HIT: AU120419-1, EVALUE 2.00e
SWISSPROT HIT: P70501, EVALUE 2.90e 02
                                                                                                                                                                                                                                                                                                                         EXPRESSED IN PLACENTA, SIGNAL - EXPRESSED IN BT474, SIGNAL 4.1 EXPRESSED IN BRAIN, SIGNAL 3.8
                                                                                                                                                                                                                                                                                                                                                                                     EXPRESSED IN FETAL LIVEF, SIGNAL = 4.3 EXPRESSED IN HEART, SIGNAL = 3.3
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                                                                                              100.0%;
                                                                           1.3%; Score 7; DB 10; Length 32; [00.0%; Pred. No. 25; [1] Indels 0; Mismatches 0; Indels
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Result
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Run on:
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                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution
                                                                     2825
2825
20124
20118
1114
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P74370 synechocyst	P74370	16	480	9.9	280
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Q91y63 arabidopsis	Q91.Y63	10	538	11.0	310
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P74334 symechocyst	P74334	16	490	14.0	ارت ۲۱ اور در
Q9m079 arabidopsis	Q9M079	10	616	15.5	437
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Q9tvb8 canis tamil	84A1.60	σ	533	37.8	1068
Q28175 bos taurus	Q28175	(J)	533	37.8	1068
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ç∪5661 bos taurus	QU5661	σ	533	37.5	1070
Q9xt71 cercopithec	Q9XT71	6	533	37.9	1070

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Q91993
Bost Coding
                                                                                                                                                                                                                                                                                      Riss G., Bachmann H., Hünzikor W.;
"Expression perfect and localization of beta beta-carotene 15,15" dicayjenase in different tissues.";
Biochem. J. 354-521-529(2001).
EMBL: AJ271386: CAB90825.1: -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-LSL LOHMANN: TISSUE-DUODENUM:
MFD(INE=21]34344, PubMed=11237856,
MFSS A., Wirtz Weggon N.D., Brugger P., Wyss M., Friedlein A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
Eukaryota; Metazwa, Chordata, Craniata, Vertebrata, Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last Sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Beta carotene 15.15'-dioxygenase (EC 1.13.11.21).
                                                                                                                  InterPro, IPRO04234, RP865, Pfam; PF03055; RP865; 1. Dioxygenase; Oxidoreductase, SEQUENCE 526 AA; 60384 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bachmann H., Hunziker W.; "Cloning and expression of beta,beta-carotene-15,15'-dloxygenase."; Exachem. Biophys. Res. Commun. 271:334-336(2000).
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MEDLINE-20261261; PubMcd-10799297;
Wyss A. Wirty G.M., Woggon W.D., Bruggor P., Wyss M., Friedlein A.,
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                         "Identification, expression and substrate specificity of beta-corotene 15,15' dioxygenase.";

I Biol. Chem. 0.0-0(2001)
EMBL; AJ278064; CAB92531.2;
EMBL; AJ278084; ACC33982.1;
MGD; MGI:1926923; Bcdol.
Interpro, IPR004294, FPE65.
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01-MAR-2001 (TrEMBLrel 16, Last sequence update)
01-JUN-2002 (TrEMBLrel 21, Last annotation update)
Beta, beta-carotene 15,15'-dioxygenase (EC 1.13.11.21).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Expression pattern and localization of beta, beta carotene 15,15'-dioxygenase in different tissues.";
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Mammalia; Eutheria; Rodontia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                            Cunningham F.X.;
                                                                                                                                                                                                                                                                                                                                                          Redmond T.M., Gentleman S., Duncan T., Yu S., Wiggert B , Gantt F
                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-C57BL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (DEC-2000) to the EMBL/GenBank/DDBT databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wyss A., Wirtz G.M., Woggon W.D., Brugger R.,
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Best Local
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STPAIN (STREE KINNEY)
Yan W., Jang G.-F., Haeseleer F., Esumi N., Chang J., Ker
Camporchiaro M., Camporchiaro P., Paleoreski K., Park D.J.;
Camporchiaro M., Camporchiaro P., Paleoreski K., Park D.J.;
Cloning and characterization of a human beta, bota carob

"Cloning and characterization of a human beta, bota carob."
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Fikaryota, Metagoa; Chordata; Craniata; Vertobrata; Eutoloostomi;
Mammalia, Eutheria, Eodentia, Sciuroamathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                    dioxygenase that is highly expressed in the retinal pigment epithelium.";
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Heta, beta-carotene 15,15'-dioxygenase (EC 1.13.11.21).
                             Dioxygenase; Oxidoreductase.
SEQUENCE 566 AA; 63852 MV
                                                                                                           MGD; MGI:1926923; Bcdol.
InterPro, IPR004294, EPE65.
Pfam; PF03055; EPE65; 1.
                                                                                                                                                                                                                                   Silmitted (AUS-2005) to the EMN Johnson Juibi databases EMBL; AF294899; AAG15381.1; -.
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                                  P 2825 WW:
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Best Local Similarity
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01-DEC-2001 (TrEMBLrei, 19, Greated)
01-DEC-2001 (TrEMBLrei, 19, Last sequence update)
01-MAR-2002 (TrEMBLrei, 20, Last annotation update)
Beta-carotene 15,15,-dioxygenase.
                                                                                                                                                                                                                                                                                                                                                                                    Takitani K., Ban R., Tamai H.;
"Regulation of beta-carotone 15,15'-dioxygenase in oxidative stress.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBI daisbases.
EMBL: AB062912; BAB60897.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota: Metacoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                   Dioxygenase
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241 VIENYVELEÖFEKI JUTKLAFAH († 1117) († 1117) († 1117) († 1117)
241 VIENYVELEÖFEKI JUTKAFAYMEGVSMASGMSEDBEDKTYTHT I DØFTEKTEVETKEY OO
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                                                                                                                                                                                                                                                                    566 AA; 63637 MW; A1FF8A47BA6CE6E5 CRC64;
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                                                                                                                                                                             75.0%; Score 2118; DB 11; 72.1%. Pred. No. 2 62-149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   epithelium."; Submitted (ANG-2000) to the EMBL/GenBank/DDRJ databases EMBL; AF294900; AAG15380.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yan W., Jang G.-F., Haeseleer F., Esumi N., Chang J., Kerrigan M., Campochiaro M., Campochiaro P., Palchowski K., Zack F.I.;
"Clouding and characterization of a human beta, beta canotene 15,15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota, Metarbar, Chardata, Crandata, Vertebrata; Enteleostomi;
Mammalia, Eutheria, Primates, Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAP-2001 (TrEMBLrel 16, Created)
01-MAP-2001 (TrEMBLrel 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Beta, beta-carotene 15,15'-dioxygonaso (FC 1 13 11 21).
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121 FORTUNINESSESYVALSEINELFELDSTELSTES VOYSEYVAVNIALSHEHYDS AGN 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                461 VPILHVDELAEVGSBLVKVSSTTATALKEKDDBVYCQDDVLYEGLELDFINYABBGKDYEY
                                                           61 TIPDGEVYYPSKYLPSDTYNTNITANDIVVSEFGTMAVPDDPCKN;FSKAPSV;SHIIPDF
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51 STEIDSEVEYESKYLGSDYYNANIEANKIVVSEEGTMAYEGEGKNIESKAESYLSHTITOE 120
                                                                                                                                                                                                                                     1 METTENKNKEEHDEDTKAEVQGQLDTWLQGVI) RNGDGMHTTGDTKYNHWEDGLALLHSE
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Submitted (PEB-200) to the EMBL/GenHank/DDHJ darabases EMHL, AKO01592, HAA91776.];
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01-007-2000 (TrEMBLIFEL 15, Last sequence update)
01-JUN-2002 (TrEMBLIFEL 21, Last amoutation update)
CDNA FLJ10730 fis, clone NT2RP3001307
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo,
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181 ILNMGTSIVDKGRTKYVLFKIPSSVPE-KEKKKSCFKHLEVVCSIPSRSLLQPSYYHSFG
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PF03055; RPE65; 1,
NCE 547 AA; 62579 MV
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Actimopterygil; Neopterygii; Teleostol; Ostariophysi; Typrimitormes;
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Kiefer C., Hessel S., Lampert J.M., Vogt K., Lederer M.O.,
Breithaupt D.E., von Liniig J.;
"Identification and characterization of a Mammalian enzyme catalyzing
the asymmetric oxidative clearage of provitamin A.";
I Biol Chem. 276:14110-14116(2001)
EMRL: A7200301; CAC37567 1: -.
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01-DEC-2001 (TrEMBLrel 19, Last sequence update)
01-MAR-2002 (TrEMBLrel 20, Last annotation update)
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Cyprinidae; Danio.
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Eukaryota: Metazoa: Chordata, Ciandala; Vertebrata, Enteleoistomi.
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                                                                                                                                             213 PKGEFYHIL-PVPPG- EKQDDDAGLSGAEILSSCHAALEFKESYYHSEVMSENYIVDIF
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43.9%; Pred. No. 9.1e
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01-DEC-2001 (fremBLrel. 19, Created)
01-DEC-2001 (fremBLrel. 19, Fast sequence update)
01-JUN-2002 (fremBLrel. 21, Last unnotation update)
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NVSLNAPEGDNLSFLSYTSASAVK@AUGTLWGSHENLH@EDLEKEGGIEFP@IYYDRESG
                                                                                QYDKDAEVGSNEVKEP ISAIAVKEKEGSIYOQPEILOE ---- GIELPKVNYD-YNG
                                                                                                                                                                 #INAPH #@CVITOTOGEWGFTLEVYCIQNLFKAGEGLECVHWSAAKCEF---RREVLPL
                                                                                                                                                                                                                                                                                                                                            IEGELKMNLWKIAISKIEGKAFSIGISWEFGINIEFHVVEKETGGILIGEYYSKETVTEH 303
                                                                                                                                                                                                                                                                                                                                                                                                                             1EQPEXLU1VKLATAY1EGVNWASGLSEHKEDRTWEHEVDRKTKKEVSTKEYTDALVLYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FGFYG-F2YKVTFVF---PEKVDLGET1HGVQVTCSTASTEKGKFSYYHSFGMTPNYTTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TVDKGRTKYVLEKIPSSVPEKEKKKSCPKHLDEVVCSIPSRSLLQPSYYHSFGITENYIVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSKYLPSCTYNGNIEANEIVVSEFGIMAYPOOGENIEAKAES YLEHTIFEETCHCLIN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EEAPFOLSAEVWOHFPKWENOSELFIGFOKFEFOKFKYNHWFFOMALLHQFFMAKGTVTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEDEPNDANTINI PYTTASAVKTATGVELYHEDLYNDHLI AYGGLEEPAINYANYNARPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1115.5; DB Pred. No. 9.2e-75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 545;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 39 4%; Score 1112.5; DB 11; Length 532; Best Local Similarity 43 5%; Fred No. 1 55 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             099NF1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kiefer C., Hessel S., Lampert J.M., Vogt K., Lederer M.O., Breithaupt D.E., von Lintig J.; "Identification and characterization of a Mammalian enzyme the asymmetric oxidative eleavage of provitamin A.", J. Biol. Chem. 276:14110-14116(2001). EMBL: AJ290492: CAC2825.1.
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Eukaryota; Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia, Sciurognathi, Muridae, Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
B,b-carotene 9',10'-dioxygenase.
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Plam; PF03055; RPE65; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIINE=21216714; PubMed=11278918;
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414 KKYKYVYATEVQWSPVPTKIAKLNVQTKEVLHWGEDHCWPSEPIFVPSPDAREEDEGVVL 473
                                                                                                                                                                                                       310
                                                                                                                                                                                                                                                                                                                                        197
                                                                                                                                                                                                                                                                                                                                                                                                                       137 QYKGDYYMSTETNFMNKVDIEMLERTEKVDWSKFIAVNGATAHPHYDPDGTAYNMGNSYG 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             501 SVVITPNQNESNELLVLDAKNFEELGRAEVPVQMPYGFHGTFIP 544
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                                                                369 DVSVDAAEGKNI.SPI.SYSSASAVKQGDGETWQSPFNI HHEDI FEEGGIEFPQINYGFFNG
                                                                                                            363 QYDKDAEVGSNLVKLP-TSATAVKEKDGSIYCQPEILCE-----GIELPRVNYD-YNG
                                                                                                                                                                                                                                              253 QPVKMKLWKIITSKIRGKPFADGISWEPQYNTRFHVVDKHTGQLLPGMYYSMPFLTYHQI
                                                                                                                                                                                                                                                                                        250 QPFKLDIVKLATAYIRGVNWASCLSFHKEDKTWFHFVDRKTKKEVSTKFYTDALVLYHHI 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               228; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 KSKFLQSDTYKANSAGGRIVISEFGTLALPDPCKSIFERFMSRFEP--PTMTDNTNVNFV 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 RSKYLRSDTYNCNIEANRIVVSEFGTMAYPDPCKNIFAKAFSYLSHTIPEFTDNCLINIM 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 EETLSAVSARVROHIPEWINGYLLRVGPGKEEFGKDRYNHWEDGMALLHQFRMERGTVTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 EEHPEPIKAEVQGQLPTWIQGVLLRNGPGMHTIGDTKYNHWEDGLALLHSETEKNGEVYY 69
                                                                                                                                                        NAFEDOGCIVIDI.CCODDGRSI.DI.YQI.QNI.RKAGEGI.DQVYEL--KAKSEP--PREVLPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                KTGDDYYATSETNFIRKIDPQTLETLDKVDYSKYVAVNLATSHPHYDSAGNILNMGTSIV 189
                                                                                                                                                                                                  NAYEEDGHVVFDIVAYRDNSLYDMFYLKK------LDKDFEVNNKLTSIPTCKRFVVPL 362
                                                                                                                                                                                                                                                                                                                                    PRG-SCYNIIPVP---PKKKEPGETIHGAQVLCSIASTEKMKPSYYHSFGMTKNYIIFVE 252
                                                                                                                                                                                                                                                                                                                                                                           DKGRTKYVLFKIPSSVPEKEKKKSCFKHLEVVCSIPSRSLLQPSYYHSFGITENYIVFIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              532 AA; 60142 MW; 7461AD5A53FE86A3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94; Mismatches 175,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q96JY5;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel 19, Last sequence update)
01-DEC-2002 (TrEMBLrel 21, Last annotation update)
01-JUN-2002 (TrEMBLrel 21, Last annotation update)
CDMA-FL-14895 fis, clone PLACE1004646, weakly similar to B.taurus
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Mammalia; Eutheria; Primates, Catarrhini; Hominidae;
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res 232; Conserv
495
                                                                  474 TCVVVSEPNKAPFLLILDAKTFKELGRATVNVEMHLDLHGMFTP 517
                                                                                                                                                                                                                        414 KKYKYVYATEVQWSPVPTKIAKLNVOTKEVLHWGEDHCWPSEPTFVPSPDAREEDEGVVI. 474
                                                                                                                                                                                                                                                                                                   382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       308 HINAYEEDGHVVFDIVAYRDNSLYDMFYLKKLDK-----DFEVNNKLTSIPICKKEVVPL
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SVV1TFNQNESNFULVILDAKNEEELGKAEVFVQMFYGFHGTFTF 538
                                                                                                                                                                                                                                                                                                   NVSLNAPEGDNLSPLSYTSASAVKQADGTIWCSHENLHQEDLEKEGGTEFPQTYYDKFSG 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                QINAFFIQGCVIII diacqiongrii evyquqini rkageglibovensaaeser — kkevilet.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIGHYG-ESYKVIKVM---PEKVDIJBIILEGVQVIJYIASIEKSKESYYHSEOMIRNYIIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVVITPNQSESNELLVLDAKSFTELGKAEVPVQMPYGFHGIEVP 531
                                                                                                                                                 KKYHFFYGCGFR-HLVGDSLIKVDVV------WFERGFYPSEPVFVPAFGTNEEDGGVIL 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IADKOSILKAATEKI Desabekekki sekati eaace theretti Operationatienatar. 747
                                                                                                                                                                                                                                                                                                                                                                         QYDKDAEVGSNLVKLP-TSATAVKEKDGSIYCQPEILCE----- GIELFFVNYD YNG 4) (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEHPEPIKAEVQGQLPTWLQGVLLRNGPGMHTIGDTKYNHWFDGLALLHSFTFKNGEVYY 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IEQPLKMNLWKIAISKIPGKAESUGISWEPQCNIFFHVVEKFIGQLLPGPYYSKPFVTFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           539 AA,
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44.3%; Pred. No. 8.4c
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5; Mismatches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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RESULT 12
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01-JHN-2001 (TrEMBLrel 17, Last sequence update)
01-JHN-2002 (TrEMBLrel 21, Last unnotation update)
Putative b,b-carotene-9',10' dioxygenase.
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Mammalia; Eutheria; Frimates; Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B-DIOX-II
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                                                                                                                                                                                                                                         414 KKYKYVYATEVQWSPVPTKIAKLNVQTKEVLHWGEDHCWPSEPIFVPSPDAREEDEGVVL 473
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512 SVVITPNONESNELLVLDAKNEEELGRAEVEVUMEYGEHGTEIF 555
                                                                            474 TCVVVSEPNKAPFILILDAKTFKELGRATVNVEMHLDLHGMFIP 517
                                                                                                                                                                                                                                                                                                                          393 NVSTNAPEGDNLSPLSYTSASAVKQADGTTGCSHENIHQEDLEKEGGTEFPQTYYDRESG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99 RSKFLQSDTYKANSAKNRIVISEFGTLALPDPCKNVFEPFMSFFELPGKAAAMTODTNVN 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 RSKYLPSDTYNGNTEANPIVVSEFGTMAYPDPCKNIFAKAFS--YLSHTIPEFTDNCLIN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39 EEAPRGISARVWGHFPKWLNGSLLRIGPGKFEFGKDKYNHWFDGMALLHQFRMAKGTVTY 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 EEHPEPIKAEVQGQLPTWLQGVLLRNGPGMHTIGDTKYNHWFDGLALLHSFTFKNGEVYY 69
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                                                                                                                                                             KKYHFFYGCGFR-HLVGDSLIKVDVVNKTLKVWREDGFYPSEPVFVPAPGTNFEDGGVIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QINAFEUQGOVIIDIA CQDNGRTLEVYQLQNLRKAGEGLDQVHNSAAKSEP--RREVLPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IEQPIKMNIMKIATSKIPGKAFSDGISWEPQONTPFHVVEKPTGQILPGRYYSKPFVTFH 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IEQPFKLDIVKLATAYIRGVNWASCLSFHKEDKTWFHFVDRKTKKEVSTKFYTDALVLYH 307
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RESULT Q91ZQ5

> RESULT 14 Q16518

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PRELIMINARY;

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01-NOV-1996 (TERMBLEE) 01. Created)
01-NOV-1996 (TERMBLEE) 01. Last sequence update)
01-DEC-2001 (TERMBLEE) 19. Last annotation update)
Rectical pigment epithelium-specific 61 kDa protein.

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091ZQ5;
01-DEC-2001
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Mammalia, Eutheria, Rodentia; Sciurognathi, Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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InterPro; IPR004294; RPE65.
Pfam; PF03055; RPE65; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (AUG-2001) to the EMBL/GenBank/NDRI databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A point mutation in Rpe65 gene causes retinal degeneration (rdl2) in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 DALVLYHHINAYEEDGHVVFDIVAYxD-NSLYDMFYEKKUDKDFEV---NNKLISTFICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 DUCLINIMKTGDDYYATSETNFIRKIDPOTLETLDKVDYSKYVAVNLATSHPHYDSAGNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 FKEGHUTYHBRFIPTDAYVRAMTEKRIVITEPGTCAFPDPCKNIFSPFESYFKGV--EVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 ETIFNENKEEHPEPIKAEVQGQLPTWLQGVLLRNGPGMHTIGDTKYNHWFDGLALLHSFT 61
VVLSVVVSPGAGQKPAYLLVLNAKDLSETAKAEVETNIPVTFHGLF
                                                                       VVLTCVVVSEPNKAP-FILIIDAKTFKELGRATVNVEMHILDIHGMF 515
                                                                                                                                                                                                                                                                                                                                 SPENLEHHINTYEUNGELIVULCCWKGEEEVYNYLYLANLKENWEEVKRNAMKAPOPEVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENY) VELEQUERIJO I VKLATAY - LEGVNWASCL SEHKED K TWEHEVDER TEKKEVSTREYT
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                                                                                                                                                                                                                 YNOKKYYYYATEY@WSTYPTKIAKLNY@TKEYLHW@EFH@WPSEPTFYPSP@AREEDEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ETV-----EELSSPLTAHVTGRIPLWLTGSLLRCGPGLFFVGSEPFYHLFDGQALLHKFD
                                                                                                                                              FGGKPYTYAYGIGINHE-VPDKICKINVKTKFIWMWQEPDSYPSEPTFVSQPDALFEDIG
                                                                                                                                                                                                                                                                                        PYVI.PITIDK-VDTGPNI.VTI PHTTATATI.RSDETTMI EDEVI ESGPRQAFEEPQI NYQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PNYIVEVETPVKINLEKELSSWSLWGANYMDGEESNESMGVWLHVADKKEREKYENNKYRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                533 N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38.18, Secre 1077, DB 11, 42.28, Fied. No. 6.5e-72; tive 89; Mismatches 191,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19,
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.ength 533;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Morimura H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nicoletti A., Wong D.J., Kawase K., Gibson L H., Yang-Feng T.L., Richards J.E., Thompson D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=RETINAL PIGMENT EPITHELIUM; MEDLINE=95359969, Pulme-d=7633413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota: Metazoa, Chordata, Craniata, Vertebiata, Eutere
Mammalia: Eutheria: Primates: Catarrhini; Hominidae: Homo-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Molecular characterization of the human gene encoding an abundant 61 kDa protein specific to the relinal pigment epithelium ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L; U20486; AAC14586.1; JOLINED.
L; AF039868; AAC39660.1; JOLINED.
L; AF039875; AAC39660.1; JOLINED.
L; AF039875; AAC39660.1; JOLINED.
AF039877; AAC39660.1; JOLINED.
AF039877; AAC39660.1; JOLINED.
L; AF039860; AAC39660.1; JOLINED.
L; AF039862; AAC39660.1; JOLINED.
L; AF039864; AAC39660.1; JOLINED.
L; AF039864; AAC39660.1; JOLINED.
L; AF039864; AAC39660.1; JOLINED.
L; AF039864; AAC39660.1; JOLINED.
L; AF039865; AAC39660.1; JOLINED.
L; AF039866; AAC39660.1; JOLINED.
L; AF039866; AAC39660.1; JOLINED.
L; AF039866; AAC39660.1; JOLINED.
L; AF039867; A
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                                        301 DALVLYHHINAYFEDGHVVFDIVAYRD-NSLYDMFYLKKLDKDFE---VNNKLTSIPTCK 356
                                                                                                                               242 ENYTYFIEQPEKLDIVKLATAY-IRGVNWASCLSEHKEDKTWEHFVDRKTKKEVSTKFYT 300
                                                                                                                                                                                 190
                                                                                                                                                                                                                    182 LNMSTSIVDKGRTKYVLFKIPSSVPEKEKKKSCFKHLEVVCSIPSRSLLQPSYYHSFGIT
                                                                                                                                                                                                                                                                   130 DNALVNVYPVGEDYYACTETNEITKINPETLETIKQVDLCNYVSVNGATAHPHIENDGTV 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROJUES: PARKS:
                                                                                                                                                                                                                                                                                                                                                             72 FKECHVTYHRRFIRTDAYVRAMTEKRIVJTEFGTCAFPDPCKNIFSRFFSYFRGV--EVT
                                                                                                                                                                                                                                                                                                                                                                                                        62 FKNGEVYYRSKYCRSDTYNCNIEANRIVVSEEGIMAYPDFCKNIEAKAFSYLSHTIPEFT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                         17
SPENLEHHINTYEDNGELIVDLCCWKGFEFVYNYLYLANLRENWEEVKKNARKAPQPEVR
                                                                                                                                                                          YNIGNCFGKNFSIAYNIVKIP---PLQADKEDPISKSETVVQFPCSDRFKPSYVHSFGLT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ETV-----EELSSPLTAHVTGRIPLWLTGSLLRCGPGLFEVGSEPFYHLFDGQALLHKFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETIFNRNKEEHPEPIKAEVQCQLPTWLQCVLLRNGPCMHTIGDTKYNHWFDGLALLHSFT 61
                                                                                       PNYIVEVETPVKINLFKFLSSWSLWGANYMDCFESNETMGVWLHIADKKRKKYLNNKYRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    533 AA; 60947 MW; 7193C93F3325798D CRC64;
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Best Local :
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"Rat mossenger RNA for the retinal pigment epithelium specific protein RPE65 gradually accumulates in two weeks from late embryonic days."; FEBS Lett. 423:133-137(1998). EMBL: AF035673: AAC40059.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-pp-2no1 (TrEMBLrel 19, Last squence update)
Retinal pigment epithelium specific protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR004294; RPE65. Pfam; PF03055; RPE65; 1.
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Mammaiia; Eutheria; Rodentia; seinrognathi; Muridae; Murinae; Rattus
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367 RYVLPLTIDK-ADTGRNLVTLPHFTATAILCSDELIWLEPEVLFSGPRQAFEFFQINVQK-425
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Search completed: July 15, 2003, 09:29:40 Job time : 88 secs

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ALIGNMENTS

RESULT 1 AAA53888 Reta, Botanianithop-15,15 dioxygenase coding sequence 03-JAN-2001 (first entry) AAA53888 standard; DNA; 3111 BP

Reta, beta-carotene-15,15-dioxygenase; vitamin A: beta-carotene; transformation; fruit; vegetable; developmental disorder; pphthalmological disorder, antibody, detection; quantification; treatment; therapy; ds.

Gallus gallus.

(HOFF) HUFFMANN DA FOOTHE & CO AG CDS 22-FEB-1999; 17-FEB-2000, 1000EF 0102289 EP1031627-A1. 36-AUG-2000. 99EP-0103382 /product- Beta, Beta-carotene-15,15 dioxygenase Location/Qualifiers /*tag= 7

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reta, beta-carotene-15,15'-dioxygenase (bCOD) is used for enzymatic conversion of beta-carotene to vitamin A and for raising specific antibodies. Nucleotides encoding all or part of bCOD are useful as primers or probes for specific amplification and/or detection of the gene that encodes bCOD, for isolation of related sequences in
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the present invention describes primer sets for synthesising 5002 full-length cDNAs defined in the specification. Where a primer set remprises (a) an object further and an objective mappinentary to the complementary strand of a polynucleotide which comprises one of the 5002 machenish sequences defined in the specification, where the obligonucleotide comprises at least 15 nucleotides or (b) a combination of 30 obligonation of the comprises at least 15 nucleotides or (b) a combination of 30 obligonation of a polynucleotide which comprises a 5 cend sequence and an obligonation of a polynucleotide which comprises a 5 cend sequence and an obligonation of the complication of a polynucleotide which comprises a 5 cend

Claim 8; SEQ ID (1971; 2537pp + CD KOM; English)

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                                                                                             Primer sets for synthesizing polynucleotides, particularly the full length etMAs defined in the specification, and for the default diagnosis of the abnormality of the proteins encoded by
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02-MAY-2000;
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27-AIIG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1025 TITACACTGATGCTITGGIGCTITATCACACATAAATGCLTACGAAGAAGATGGCCACG T084
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AAH42170;

17-SEP-2001 (::rst entry)

Nucleotide seguence of a terrarian construction (trial few)

transgenic plant; Beta-carotene dioxygenase; beta-diox; beta carotene; vitamin A aldebyde: transgenic plant; ss.

Danio rerio

Location/Qualifiers 94..1644

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence encodes a beta-carolene dioxygenase (beta-diox) polypeptide. Beta-diox specifically cleaves beta-carolene to form vitamin A aldehyde. Beta-diox is is useful for producing transgenic plants. The transgenic plants have improved morritional quality or physiological condition and accumulate vitamin A aldehyde and can take up beta-carotene from the medium. Expression systems encoding beta-diox activity. Identification of cDNAs encoding beta-diox allows the physiological characterization of cDNAs encoding beta-diox allows the physiological characterization of mammalian vitamin A metabolism. Vitamin A production in crops and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dioxygenase (beta-diox) protein that cleaves beta carptene to form vitamin A aldehyde, and polynucleotides encoding them useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1773 BP; 556 A; 360 C; 406 G; 451 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; Page 83-86; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        producing transgenic bacteria, fungi, plants expressing the polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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552 GACTAACTTCATCAGAAAAATTGATCCACAGACTCTGGAGACACAACTAGATAAGGTAGACTA 611
                                                                                                                                                                                                                                                                                                              273 TGCAATTAATAAAGGAGGGGGAGGTACAGGAGGAGATATCTTCGAGGTGACACCTATAA
                                                                                                                                                                                                                                                                                                                                                                                                     192 GCAAGGTCAGTTGCCCACTTGGTTGCAAGGGGTACTTCTCCGAAATGGCCCAGGGATGCA 251
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                                            CACTGACAACTGTGGGAATAACATAATCAAATATGGAAATGACTTCCATGCTACGTCTGA
                                                                                    CACGGACAACTGGCTGATCAACATTATGAAAACTGGGGATGATTATTATGCTACCAGTGA
                                                                                                                                CCCATGCAAAAACATATTCTCCAAAGTGA LCACCTTCCTCAGCCACACCAGCCGAGACCA
                                                                                                                                                                        TCCATGCAAAAACATATTTGCCAAGGCATTCTCALACTTATCTCACACCATTCCTGAGTT
                                                                                                                                                                                                                       CTCCAACATGCAGGCCAACAGAAAAAGTAGTAGTAGGAGATGGGGAGCATGGCGGGA
                                                                                                                                                                                                                                            CTGCAATATAGAAGCAAACCGAATCGTGGAGTTTGGGATTTGGAACCATGGTTTATCCGGA 431
                                                                                                                                                                                                                                                                                                                                                        CACGITTAAAAATGGTGAAGITTACTACAGAAGTAAGTACCTCCGAAGTGACACATACAA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAGGGCTCGATTCCTGAATGGGTGCAGGGAACACTAATAGGCAATGGACGCGGCATGTT 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATGCAGTACGACTATGGCAAAAAACAAGGAAGAACATCCGGAGCCCATCAAAACTGAAGT 152
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/product= "beta-earotene dioxygenase (beta-diox)"
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Pred. No. le-131
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                1632 AURICAGASTTAAGGTAGAAATGTATGTGGAGGTATGGGATGTTTATAGCAGAATGA
                                                                                                                                                                                                1164 TUUUUTTAGTGAGGGTGAGACAGGTGAGGATCTGGTCAAACTTAAATACACAA----C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1092 TGATATCGTTGCCTACAGAGACAATAGCTTGTACGATATGTTTTACTTAAAAAAACTGGA 1151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  867 CACGGCITAITTGAGGAGGGIGAGCTGGGCCAGCTGCAIGAAGIIIICACCCIGAAGACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              912 AACTECTACATOCIAGATATAAASTATAAACTEGATECTETOCII FTATAAAAAAGAAGATAA 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       807 GACCGACAACTACLICATCTICAICGAGCAACCCTIGAAGCIGGALATCCTAAAAATGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               747 Transfer Andrina mentranda percepentra menerakan Tantan (Adam trinsen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        693_GGTCC=====CAGGAGGAAGCAGGCAGGCTGGACCTTTGAAAAGGCCTGAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             612 CAGPAAATA IGTAGCIGTAAACH IGGCAACHIO I CACCCAGACTATGACACTGCIGGAAA 671
                                                                                                                                                     CAGGCCERTFGAGGAFGAAGATGATGGFGT AGTTCTGACAGTTATCATTAATAACAA
                                                                 ACCTOTG/TAGGGI GGCI FTOT ACT/GATGGCTTGATGGCAAGTCTTTCAAAGAGATT GCCCC
                                                                                    GCCAAA1AAAGCAGGCIAGCIGACTGATGTT6GATGGTAAAAAAATA11GAAAGAA11G36GCG
                                                                                                                                                                                                                                            AAAGCAGCAGATTGAGTGGAAAGGAAGTAATTTTTGCATCAGAGCCCGTTTTCATTCC
                                                                                                                                                                                                                                                                                    AAAGGAAGTACTGCACTGGGGAGAAGACCACTGCTGGCCCTCAGAGCCCATCTTTGTTCC
                                                                                                                                                                                                                                                                                                                                     CATGIST TSTSTAGASGAATSSCSSAGTASGASTALTS (SAAGTITSATSS SAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCAAGTGCTGTGAAGGAGAAGATGGGGAAAATAATGTGTCAGGAGAGGTTCTATGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGCAACTGCTGTAAAAGAAAAGATSGCAGCATCTATTGTCAACCTGAAATATTATGTGA 1331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAAAGACTTTGAAGTGAACAACAAGCTTACCTTCATCCCAACCTGCAAGCGCTTTGTTGT 1211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGATGCAATGACCGTCTACCATCAAGTCAATGCCTTTGAAGATGATGGGGCATGTTGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACAGAAAATTATATTGTTCATAGAGCAGCCATTTAAACTGGATATIGTCAAACTGGC
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                                                                                                                                                                                                                                                                                                                                                                           TGCAACAGAAGTCCAGTGGAGCCCAGTCCCTACAAAGATLGCAAAACTGAATGTCCAAAC 1451
                                                                                                                                                                                                                                                                                                                                                                                                                          AGGINTIFICAAACITECCAAGAATTAAFTACAACITICAATGGAAAGAAGAAGTACAGATATTCATA 1340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCTCTGCAGTATGACAAGAATGCAAAAGTAGGTCTCTAATTTAGTCAAACTTCCAACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGAGACGA1GGGAG---CAACAAAITIGIACIGCAAACCCAAGTTCACAAGATTTGTGTT 1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGATGTGATTGCCTATGATGACAACAACTTGTATGAATTCTTTTTACCTGAACAAACTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THATH TITGHTH OTTATION 'ANALASTA' THAN SAAGAAGA IGHILAGGITHTT
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RESULT 4
AAHOGAA
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                                                                                                                                     complementary straind of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detertion and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs assily without any specialised methods. AAH03166 to AAH13628 and AAH13633 represent human cDNA sequences; AAB92446 to AAH13639 represent human cDNA sequences; AAB92446 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the 5602 nucleotide sequences defined in the specification, where the oliqonucleotide comprises at least 15 nucleotides; or (b) a combination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes primer sets for synthesising 5602 full length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDMAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                      represent oligonariestides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of an oligonucleotide comprising a sequence complementary to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to the complementary strand of a polynucleotide which comprises one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ 1D 3313; 2537pp + CD ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HELL -) HELLX RES INST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JUL-2000; 2000EF-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP1074617-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cDNA clone (5'-primer) SEQ ID NO:3313,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH06478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH06478 standard; cDNA, 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1641 CTGAGGGTTTGA 1652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1999;
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T, Wakamatsu A, Nagai K,
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Sequence 809 BP; 257 A; 183 C; 215 G; 151 T; 3 other;
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10.7%;

Score 333.4;

DB 22; Length 809;

07-OCT-1999; 12-NOV-1999;

9908-0165192 99US-0158578 9908-0145232

21-JUL-1999;

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                                                                                                                              01-FEB-2001
                                                                                                                                                                                                                                                                                          neetropic: neuroprotective; anticonvalsant; antiparkinsonian; anti-HIV; antidiabetic; immunostimulant; immunomodulator; antiinflammatory;
                                                                                       21-JUL-2000; 2000WO-HS20035
                                                                                                                                                                 W0200107612-A2
                                                                                                                                                                                                                                         antiarteriosclerotic;
                                                                                                                                                                                                                                                       antithyroid; immunosuppressive; nephrotropic; antiqout; thyromimetic; cytostatic; antibacterial; virucide; fungicide; protozoacide;
                                                                                                                                                                                                                                                                                                                               Human; RECAP; receptors and associated proteins; cerebroprotective;
                                                                                                                                                                                                                                                                                                                                                                    Human RECAP polynucleotide, SEQ ID NO: 24.
                                                                                                                                                                                                                                                                                                                                                                                                       24-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAr58596 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       274 AAGTGACAGGCAAGATTGCAGCATGGCTGCAGGGAACCCTTGCTCCGCAATGGGCCTGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 GAGCAATGGATATAATATTTGGCAGGAATAGGAAAGAACACCTGGGGGCTGTGAGGGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 AGNERAAGNEVARTEGREEN LGCTEGRAAGNESTACITETECGAAATGGCCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 GAGCGATGGAGACAATATTTAACAGAAACAAAGAGGAGCGTCCAGAGAGCCCATAAAAGCTG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GJAAATSTTOTAAACATGGGCCCCATTCANTTGGGGGAAAANGGGGAAAAACCAAAAT 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGGATCCATGCAAAAACATATTTGCCAAGGCATTCTCATACTTATCTCAAACAATTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTATEGTAAATAEGTGGEGGTAAATETTGGEAACGTEACATNEECATTATGATGAAGET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGAGACCAATTACATCAGGAAAATCAACCCACAGAGACTCTGGAAACCCCTGGAGAGGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGAGACTAACTICA1CAGAAAAA11GA1CCACAGAG1C1C1GGAGACACTAGATAAGG1AG 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTTCACAGACAACTGCCTGATCAACATCATGAAGTGCGGAGAAGACTTCTACGCGACCT 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGGACCCCTGCAAAAACATAITITCCAAAGCITTCTCCTACITGTCTCACACCAICCAICCCG 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACAACACCAATAITGAGGCAAACAGGATTGIGGFGTGTGAGTTIGGAACAATGGCCTATC 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGCACACAGTTGGGGAGTCCAGATACAACCATTGGTTCGACGGCCTTGCCTGCTCCACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGTTCACGGACAACTGCCTGATCAACAFTATCAAAACTGCGGATGAFTATTATGCTACCA 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTTCACCATCAGAGACGGTGAAGTCTATTACAGGAGCAAATACCTGAGAAGCGATACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hepatotropic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2051
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0; Mismatches 149;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  syndrome); immunological disorders, including autoimmune/inflammatory disorders such as AIDS. DiGeorge's syndrome, every combined immunodeficiency disease (SCID). Chediak-Higashi syndrome, Cushing's disease, Addison s disease, autoimmune thyroiditis, Crohn's disease, disease, autoimmune thyroiditis, Crohn's disease, disease, autoimmune thyroiditis, Crohn's diseases, Hashimoto's thyroiditis, Sjugren's Syndrome, Werner's Syndrome, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections; and cell proliferation disorders such as arteriosclerosis, atherosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proteins) polypeptide. RECAP polynucleotides and polypeptides are use in the diagnosis, treatment and prevention of neurological disorders such as stroke, Alzheimer's disease, Pick's disease, Huntington's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel receptors and associated proteins for diagnosis and treatment of neurological disorders, immunological disorders including autoimmune/inflammatory disorders and cell proliferative disorders such as cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lateral sclerosis, multiple sclerosis, bacterial and viral meningitis, CJD (Creutzieldt Jakob disease). GSS (Gerstmann -Straussler-Scheinker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease, dementia, Parkinson's disease, Downs's syndrome, amyotrophic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 115-116; 128pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2051 BP; 578 A; 412 C; 508 G; 553 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cirrhosis, hepatitis and cancer.
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Baughn MR,
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  758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160 GAAGAGCATCCAGAGCCCATAAAAGCTGAGGTGCAAGGTCAGTTGCCCACTTGGTGAA 219
  GGAGCAACTGCACATCCTCATTATGACCCGGATGGAACAGCATACAATATGGGGAACTCC
                                             TTGGCAACTTCTCACCCACACTATGACAGTGCTGGAAATATTCTCAACATGGGTACTTCA 693
                                                                                                 GACATTGAAACTCTGGAAAAAACAGAAAAGGTAGATTGGAGCAAATTTATTGGTGTGAAT
                                                                                                                                                    GATCCACAGACTCTGGAGACACTAGATAAGGTAGACTACAGCAAATATGTAGCTGTAAAC 633
                                                                                                                                                                                                       TATGTGCGGTACAAGGGTGATTACTACCTCTGCACTGAGACCAACTTTATGAATAAAGTG
                                                                                                                                                                                                                                                        ATTATGAAAACTGGGGATGATTATTATGCTACCAGTGAGACTAACTTCATCAGAAAAATT 573
                                                                                                                                                                                                                                                                                                                                                         AAGGCATICICALACLIAICTCACACCAITECTGAGTTCACGGACAACTGCCTGATCAAC 513
                                                                                                                                                                                                                                                                                                                                                                                                             ATCTCAGAALLUGGGACACIGGCTCTCCCGGAFCCALGCAAGAATGTTTTTTGAAACGTTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAGAGGCICCACGGGGAAICHCIGCICGAGTCIGGGGACAFITTCCIAAGIGGCICAAF 337
                                                                                                                                                                                                                                                                                                           ATGTCCAGG ( ) GAGC FGCCTGGTAAAGCTGCAGCCATGACTGACAACAATACTAATGTCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGAAGTAAGTACCTCCGAAGTGACACATACAACTGCAATATAGAAGCAAACCGAATCGTG
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Patterson C, Lal P;
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                                                                           1681 CC
                                                                                                                                                                          1621 GAATTGGGCCGAGCCACAGTTAACGTAGAAAHGCAFCTGGACCFGCALGGGALGHTFATA 1680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 866 AASGTGGACCTTGGGGAGACAATCCATGGAGHCCAGGTGATATGCTTCTATTGCTTCTACA 925
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                                                                                                                            GASCTGGGCCGAGAGAGGTACCTGTGCAGATGCCTTATGGGTTCCAIGGIACCTTCAIA
                                                                                                                                                                                                                                ATCACTCCCAACCAGAATGAAAGCAATTTTCTCCIAGTITTGGATGCCAAGAACIIIGAA
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02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                             detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods, AAH3316 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences, AAB92446 to AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligo-nucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination
                                                                                                                                                                                                                                          Sequence 1983 BP; 583 A; 384 C; 493 G; 523 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the specification. The primer sets can be used in antisense therapy and in gone therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primer sets for synthesizing polynucleofides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosts of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                          of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 8; SEQ ID 12717; 2537pp + CD ROM, English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tull-length cDNAs -
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27-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cDNA sequence SEQ ID NO:12717
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                                                                                                                                                         Local Similarity
184 GAAGAGATTOCACGGGGGATOTOTGCTOGAGTCTGGGGACATTTTCCTAAGTGGCTCAAT 243
                                                   160 GAAGAGCATCCAGAGGCCATAAAAAGCTGAAGGTGCAAGGTCAGTTGCCCACTTGGTTGCAA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sugiyama
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2000JP-0183767
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51.1%;
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T, Wakamatsu A, Nagai F
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                                                                                                                                                      Score 272.8; DB 2
Pred. No. 8.2e·57;
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K, Otsuki T;
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                      1252 AGTITGAATGCCCCTGAGGGAGACAACCTGAGTCCATTGTCCTATACTTCAGCCAGTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1054 CACATAAATGCTTACGAAGAAGATGGCCACGTTGTTTTTGATAT------CGTTGCC | | 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     754 AAAGAAAAGAAACTIGTTTTAAACACTGGAAGTAGTATGCTCCATCCCTTCTCGC 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      484
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                                                                                   GACAAGGATGCAGAAGTAGGTTCTAATTTAGTCAAACTTCC
                                                                                                                                                                                                             GTGAACAACAACHTACCTCCATCCCAACCTGCAAGCCCTTGTF01GCCFT3GCAGTAT 1224
                                                                                                                                                GGAAGAACCCTAGAAGTTTACCAGTTACAGAATCTCAGGAAGGCTGGGGAAGGGTTGGAL 1191
                                                                                                                                                                                                                                                                                                                                                                                             CAAAHCAARGCCTI IGAGGACCAGGGCIGI GI HAFAA ITGATTI GI GCTCH CAAGATAAT HHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAACGCACTGGACAGCTCCTTCCAGGGAGATACTACAGCAAACCTTTTCTTACATTTCAT 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGAAAGACGAAAAAAGAAGTATCCACCAAGTTTTACACTGATGCT11GGTGCTTTATCAC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AACTGGGCTTCCTGCCTTTCCTTTCATAAGGAGGATAAGACGTGGTTTCACTTTGTAGAC 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATAGAGCAGCCAIIIAAACIGGATAIIGICAAACIGGCAACIGCCTACAICCGAGGTGTG 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGAAAGGGAAACCTICTIACIACCATAGCTITUGAATGACAAGGACTATATAATTITC 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTS ------GGCCATATGCTTTC (CCTATAACGTTATTCCCC) TCCTCCACAC
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                                                                                                                                                                                                                                                                                                                                TACAGAGACAATAGCTTGTACGATATGTTTACTTAAAAAAAQTGGACAAAGACTTTGAA T164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TATGTGCGGTACAAGGGTGATTACTACCTCLGCACTGAGACCAACTTTATGAATAAAGTG
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QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tycopene, beta apocarotenal; beta ionone, apolycopenal; grain seed; corn; oil seed, palm, chick pea; diagnostic, therapeutic, ribozyme, retinoid/vitamin A deficiency, beta diox il transpenio: nutrition;
        Novel isolated mouse, human, zebrafish beta-carotene dioxygenase (beta-diox II) protein that cheaves beta earntene and lycopene to yield beta apocarotenal and beta-ionome, and apolycopenals, respectively
                                                                                                                                                                                                                                                                                     05-JUL-2001
                                                                                                                                                                                                                                                                                                                   WO200148163-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     carotene/retinoid pathway; vitamin A aldehyde; retinoic acid; crop;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beta-carotene dioxygenase; beta-diox I; human-2; beta carotene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAS07196 standard; cDNA; 1934 BP
                                                                                               WPI; 2001-425657/45.
                                                                                                                                                              (GREE-) GREENOVATION PELANZENBIOTECHNOLOGIE GMBH
                                                                                                                                                                                                  20-MAR-2000: 2000EP-0105822
                                                                                                                                                                                                                                                 27-DEC-2000; 2000WO-EF13273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding human-2, beta-carotene dioxygenase (Beta-diox II).
                                                                                                                                                                                                                   24 - PEC - 1999 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1672 GTACCTGTGCAGATGCCTTA1GGGTTCCATGGTACCTTCATACC 1715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1432 TATCATTTCTTTTATGGCTGTGGCTTTGGGGATTGAGTGGGGGATTCTGTGATGAAGGTT 1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1402 GTCCAGTGGAGCCCAGTTOUTADAA---AGAFFGAAAAACTGAATGFCCAAADAAAGGAA 1458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1312 GTGAAACAGGCTGATGGAACGATCTGGTGCTCTCATGAAAATCTACATCAGGAGGACCTA 1371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1282 GTAAAAGAAAAAAGATOGGAGCATOTATTTTCAACCTGAAATATTATGTGAAGGGATAGAA 1341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTTAACGTAGAAATGCATCTGGACCTGCATGCATGTTLATACC 1682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAGCACCCTTCCTACTCATCTTGGATGCTAAAACATTCAAAGAATTGGGCCGAGCACA 1638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATGCAAGAGAAAGGATGAAAGTGTTGTTTTTAACCTGTGTTGTTGTTGTTGTTGTTGTTGTAGCCAAAT 1578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTACTGCACTGGGGAGAAGACCACTGCTGGCCCCCAGAGCCCCAFCCTGGTGCCCAGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAAAGGAAGGAGGCATTGAATTTTCCTCAGATCTACTATGATCGATTCAGTGGCAAAAAG 1431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                               Vogt K;
                                                                                                                                                                                                                  99EP-0125895
                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/product="Human-2"
                                                                                                                                                                                                                                                                                                                                               /note= "Beta-carotene dioxygenase (beta-diox 11)"
                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualitiers
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a cell or tissue which can modify the level of vitamin A and other retinoids. Antibodies are useful for studying beta-diex I: localisation, screening of an expression library to identify nucleic acids encoding beta-diex II or the structure of functional domains. The transgenic fungi, yeast, insect, animal or plant cells, seeds, tissues, or whole organisms have improved nutritional quality or physiological condition and accumulate important metabolites of carotene/retinoid pathways such as vitamin A aldehyde and retinoic acid, ceta-carotene or take up beta-carotene from the medium Expression systems encoding beta-diex II are
                                                                                                             useful in the study of beta-diox II activity. Identification of cDNAs encoding beta-diox I and II allows the physiological characterisation of mammalian carotene/retinoid metabolism. Vitamin A production in crops and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          determining the presence of quantity of beta-diox II morbels acid and determining presence and amount of beta-diox II. The polypeptide is a useful for increasing or decreasing the amount of beta-diox II levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful as probes and as a guideline to define new PCR (polymerase chain reaction) primers for the cloning of substantially homologous DNA segmences from other sources. The north-reacids are also useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                endogenous beta-diox II. The beta-diox II specific antisense oligonuclectides derived from the DNA sequence are useful for dose response studies in relevant models of retinoid/vitamin A deficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence represents the coding sequence of human-2, beta-carotene dioxygenase (Beta-diox II). Beta-diox specifically cleaves beta-carotene and lycopene to form beta-apocarotenal and beta-innone, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for diagnostic and/or therapeutic purposes and for preparing antisense or riberymo type therapeutic agents and for detecting any absormality of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         apolycopenals, respectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; Page 111-113; 115pp; English
Sequence 1934 BP; 553 A; 383 C; 477 G; 521 T; 0 other;
                                                           with the cDNAs.
                                                                                       microorganisms can be achieved by transforming the organisms or crops
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             during any stage of an organism's development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 carrots, sweet potatoes, sugar beets, banana. The polypeptide is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   edible seeds or seeds with edible parts e.g. chick-peas; potatoes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   corn;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The DNA is useful for transforming grain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brassica seeds; edible seeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The nucleic acids are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .g. palm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          also
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Query Match 8.8%; Score 272.4; DB 22; Length 1934; Best Local Similarity 51.2%; Pred. No. 1e-56; Matches 800; Conservative 0; Mismatches 711; Indels 51; Gaps 5;

QY 5 ž 3 ÇΥ Дb Qy DЬ Ę G G Š DЬ 535 GACATTGAAACTGTGGAAAAAAGAGAAAAAGGTAGATTGGAGCAAATTTATTGCTGTGAAT 594 454 AAGGPATHCHCATACTIANCHCACACPATHCC GAGTHCACAGAACACCTGCCTGATCAAC 513 400 GTGTCTGAGTTTGGAACCATGGCTTATCCGGCATGCAAGAAAACATATTTG-----CC 220 0000 PARTER TECCOAAA I ROCHCAGOTA POPACACAA I AGROGACIACIAAAT ACCAC 279 115 GAAGAGACTOCACGGGGCATOTOTGCTOGAGTOTTGGGGACATTTTCCTAAGTGGCTCAAT 160 - БААБАБЛАТОМАНАБЛОМАТАЛАААБЛОТБАЛАТБІЛААБЛІСАЯТТЯГГГАСТТЯГТТЯГАА - 219 574 GATECACAGACICTGGAGACACTAGATAAGGTAGACTACAGCAAATATGTAGCTGTAAAC 633 ATTATGAAAACTGGGGATGATTATTATGCTACCAGTGAGACTAACTTCATCAGAAAAATT 573 TRAPETERAPHARTATEPSATER STEECACACTEPSACETEFAAAAAFIGETGAAGTTTACTAC TATGTGCGGTACAAGGGTGATTACTACCTCTGCACCGAGACCAACTTTATGAATAAAGTG ATGTOCAGGTT1GAGC1GCCGGGTAAAGC1CCAGCCA FGACFGACGATACTAATGTCAAC AGAAGTAAGTACCTCCGAAGTGACACATACAACTGCAATATAGAAGCAAACCGAATCGTG GGC FC FC FACT FCGAA FTGGAACTGGGAAAFTFCGAGAAGTTTGGGAAAGGATAAGTACAATCAT AGGAGCAAGTTTCTACAGAGTGATACATATAAGGCCAACAGTGCTAAAAAACCGAATTGTG 453 354 399 294

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                                                                                                      1543 ATCACTCCCAACCAGAATGAAAGCAATTI ECICCLAGTITIGGA IGOCAAGAACITTIGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1165 GTGAACAACCAAGCTTACCTCCATCCCAACCTGCAAGCGCTTTGTTGTGCCTCTGCAGTAT 1224
1603 CACCTCGGCCGAGGGAGAGGTACCTGTGCAGATGCCTTATGGGTTCCATGGTACCTTCATA
                                                                                                                            | 1561 | CTGATTOTOTGAGOOAAATAAAGOAOOOTTOGTAOTOTTTGGATOTTTGGATOTTAAAACATTOAAA 1620
                                                                                                                                                                                                                                                                                                                                                                       1441 AATGTCCAAACAAAGGAAGTACTGCACTGGGGAGAAGAGCCACTGGTGGGCCCTCAGAGGCC 1500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1243 GTGAAACAGGCTGATGGAACGATCTGCTGCTGTTATGAAAATCTACATCAGGAGGAGGACCTA 1302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1123 CAGGTCCATAATTCAGCAGCCAAATCIITCCCICGAAGGTIIGIIITGCCTTTAAATGTC 1182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1054 CACATAAATGCTTACGAAGAAGAIGGCCACGTFGFFFFFFGAIAT------CGTTGCC 1104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     994 AGAAAGACGAAAAAAGAAGTATCCACCAAGTTTTACACTGATGCTTTGGTGCTTTATCAC 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          883 GCCTTTTCAGATGGGATAAGCTGGGAACCCCAGTGTAATACGCGGTTTCATGTGGTCGAA 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           823 ATTGAACAACCTCTAAAGATGAACCTGTGGGAAAAFIGCCACIICTAAAATTCGGGGAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               874 ATAGAGCAGCCATTTAAACTGGATATTGTCAAACTGGCAACTGCCTACATCCGAGGTGTG 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     814 TCCCTGCTCCAACCAAGCTACTACCACAGCTTTGGAATCACAGAAAATTATATTGTGTTC 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          703 GAGGTGGACCTTGGGGAGACAATGCATGGAGTGCAGGTGATAIGTTCLATTGCTTCTACA 752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         634 TRUCCAACTTCTCACCCACACTATGACAGTGCTGGAAATATTCTCAACATGGGTACTTCA 693
                                               DAAT KUMOTTAGOTTAGASTTAACHTAGAAATSTATTIGGACCID TATAIDDALIIIIIIIATA LIKU
                                                                                                                                                                                                            ATCTTTGTTGCCAGGCCCGATGGAAGAGAAGAGGATGAAGGTGTTGTTTTGAGGTGTGTTT 15mm
                                                                                                                                                                                                                                                                                                                   CATGTGGTGAATAAGACACTGAAGGTTTGGAGAGAAGATGGCTTTTATCCCTCAGAACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UACAAGGATGCAGAAGTAGGTTCTAATTTAGTCAAACTTCC---AACTTCCGCAACTGCT 1281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 8.5%;
Best Local Similarity 52.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence encodes canine retinal plument epithelium 65 (RPE65) which has a sequence of 533 amino acids defined in the specification. The gene is useful for identifying dogs which are genetically normal, or are carriers of, or affected with congenital stationary night blindness (CSNB). Carriers for CSNB are identified through the detection of an AAGA deletion at nucleotides 487.490 in the canine RPE65 gene. This allows a breader to eliminate the carrier from the breeding stock or to breed carriers with recetically formal loss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1724 BF; 465 A; 421 C; 394 G; 444 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 1A-1B; 25pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acid molecule encoding canine retinal pigment epithelium 65, where presence of mutation in one or both alleles is indicative of a carrier of, or dog affected with congenital stationary night
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Canine, dog, RPE65, canine retinal pigment epithelium 65; RPE65; congenital stationary night blindness; CSNB; mutation detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-OCT-1998;
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                                                        273 CAACCACTOSTITUGATIQUCTITICCCTCCCACACCTTCACCTTTAAAAATGCTCAAGT 332
                                                                                                                                                                                                                    213 GEFGCAAGGGGTACTTCTCCCAAALCGCCCAGGCAFCACACAATAACAGAACTAAACA
                                                                                                                                                                                                                                                                                                                                                            GCTCACGGGCAGTCTCCTCCGA1GCGGACCCGGGGCTCTTCGGGGGTTGGGATCTGAACCATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                        0. Mismatotes 702,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 264.8; DB 2
Pred. No. 7.2e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22; Length 1724;
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L58 CACCTATCACAGAAGGTTCATCCCCCACCGATGCTTACGTCCGGGCCAATGACCGAGAAAAAG

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1203
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                                                                              1323 GTACCCGTATGGACTTGGCTTGAATCACTECCTECCGGACACCTCTGCAAGCTGAACGT 1382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1221 GTATGAGAAGGAGGAGAAGTAGTI TAALLIAGIGAAAGTI FOO - AAGTGGGGAAAG 1277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1050 TCACCACATAAATGCTTACGAAGAAGATGGGCCACGTTGTTTTTGATATCGTTGCCTT---A 1106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                963 CTATTATATATAATATTIANSAASACAATGAGTITOTBATESINGGATOTOTBOTGOTBOAA 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              903 TRACAAAAAAAAAAAAATATATRAATAATAAGIARAGIARKEEEEEETTTAAIGEET 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  453 CAAGGCATTCTCATACTTATCTCACACCATTCCTGAGTTCACGGACAACTGCCTGATCAA 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGATTTGAATTCGTCTACAATTACTTGTATTTAGCCAATTTACGTGAGAACTGGGAAGA 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAAGAAAAGAAATCTTGTTTTAAACACCIGGAAGTACTAIGCICCAICCCTCCCG 812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAATCCTGAGACCCTGGAGAGAATTAAGCAGGTTGATCTCTGCAACTAGGTCTCTGTGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATGGTGGTGTC1GAA3TTTGGSAACCATGGGTTATGGGGATCCATGCAAAAACATATTTGC
                                                                                                                                                                                                                                   TOGECAAGCCTTTGAGTTTTCCTCAAATCAACTATCACAAGTATGGCGGAAGCCTTACAC 1 czz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGACCGATTCAAGCCATCGTACGTCCATAGTTTTGGTTTGACTCCCAACTATATTGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAATATCGACAAGAGGCCGACAGAGAGAAGAAGCLAGTCAGCCTTCCCAACACGACGGCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAACAACAAGCTIACCICCAICCCAACCIGCAAGCGCITT-----GTIGIGCCTCTGCA 1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCCAACTACATGGATTGTTTTGAGTCCAATGAAACCATGGGGTTCAGATCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATAGAGCAGCCATTTAAACTGGALALTGTCAAACTGGCAACTGCCLACA----1CCGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGATCCACAGACTCTGGAGACACTAGATAAGGTAGACTACAGCAAATATGTAGCTGTAAA 632
                                                                                                                                                IGICIAIGZAACAGAAGICCAGIGGAGECCAGITCCTACAAAGATTGCAAAACTGAATGT 1445
                                                                                                                                                                                                                                                                                                              TGCAACTCTTGCGCAGCCAACAACACCTCTCGCTGGGAAACCTGAGGTTCTCTTTTTTCTCAGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGCTGTAAAAGAAGAAGGCAGCATCTATTG1CAACCTGAAATATTAT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTGAAAAAAATGCCAGAAAAGGCTCCGCAGCCTGAAAGTTAGGAGCCGGTGCCGTGCCTTTT 11142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTGAACTGGGCTTCCTGCCTTTCCTTTCATAAGGAGGATAAGACGTGGTTTCACTTTGT 989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGTGGAGACGCCAGTCAAAATTAACCTGCTCAAGTTgCTTTCgtpGctpGaGtcTtp3636
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The sequence represents the coding sequence of wase 2, beta carotene dioxygenase (Retardiox II). Reta diox specifically cleaves beta carotene and lycopene to form beta appearance and beta income, and applyopenals, respectively. The DNA is useful for transforming grain seeds, e.g. corn, oil seeds, e.g. Riasira seeds; edible seeds of palm, edible seeds of seeds with edible parts e.g. chick peas; potatoes, carrots, seet potatoes, sugar beets, benana. The polypeptide is useful for diagnostic and/or therapeutic purposes and for preparing antisonse or ribozyme type therapeutic agents and for detecting any abnormality of

palm;

Claım 8; Page luz lu4; Ilépp; English

beta-apocarotenal and beta-ionone, and apolycopenals, respectively

endogenous beta-diox II.

The beta-diox II specific antisense from the DNA sequence are useful to

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heta carotene dioxygenase: bota-diox I; mouse-2; beta-carotene: lycopene, beta-dp-parotenal, beta-innovae, apolycopenal; grain seed, oil seed; palm; chick-pea; diagnostic; therapeutic; ribozyme; retinoid/vitamin A deficiency; beta-diox II; transquare; nutrition; carotene/retinoid pathway; vitamin A aldehyde; retinoic acid; crop;
                                                                                                                                                                                             Nevel isolated muse, human, metaffsh beta-car deno di expense (beta-diox II) protein that cleaves beta carotene and lycopene to yield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AASU7194 standard, cDNA,
                                                                                                                                                                                                                                                   WPI; 2001-425657/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENA encoding mouse-2, heta-carotene dioxygenase (Beta-diox II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-OCT-2001 (first entry)
                                                                                                                                                                                                                                       F-PSDB; AAU04292.
                                                                                                                                                                                                                                                                              Von Lintig J,
                                                                                                                                                                                                                                                                                                         (GPEE-) GREENOVATION PELANZENBIOTECHNOLOGIE GMBH
                                                                                                                                                                                                                                                                                                                                  EU MAR-1000; 1000EF-0105822
                                                                                                                                                                                                                                                                                                                                                (666-1361-12
                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                             W0200148153-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1503 COCTEGEGGAGGACAAAAGCCTGCTTATCTTCTGATTCTGAATGCCAAGGATTTGAGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1506 - раучесте Адрекета нас Адаска Аналия (Аналия) на пете пете пете се постава на претитува (Ст. 1565)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGETGCCAGGGCTGAAGGGACCATTAACATCCCTGCACCTTTCATGGACTGTTCAAA 1620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTTTCTCACCCAGATGCCTTGGAAGAAAATGATGTGTAGTTCTGAGTGTGGTGGTGAG 1502
                                                                                                                                                                                                                                                                                                                                                 はいだけ このしいかばない
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Beta-carotene dioxygenase (beta-diox II)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "Mouse-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag=_a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1855
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Matches 806;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       determining presence and amount of beta-diox II. The polypeptide is also useful for increasing or decreasing the amount of beta-diox II levels in a cell or tissue which can modify the level of vitamin A and other retinoids. Antibodies are useful for studying beta-diox II localisation, screening of an expression library to identify nucleic acids encoding beta-diox II or the structure of functional domains. The transgenic lungi, yeast, insect, animal or plant cells, seeds, tissues, or whole organisms have improved nutritional quality or physiological condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   response studies in relevant models of retinoid/vitamin A deficiency during any stage of an organism's development. The nucleic acids are also useful as probes and as a guideline to define new PCR (polymerase chain reaction) primers for the cloning of substantially homologous DNA sequences from other sources. The nucleic acids are also useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1855 BP; 502 A; 404 C; 482 G; 467 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            determining the presence or quantity of beta-diox II nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              with the cDNAs
637 GAGGCCGGGGAGGALLGAGGGAGGAGAGAGATESTATIGTEGCATEGGCTCVACEGAAAAA E96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         640 ACTTCTCACCCACACTATGACAGTGCTGGAAATATTCTCAACATGGGTACTTCAATTGTT 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   409 CAGTACAAAGGTGATTACTACATGAGCACAGAGACTAATTTTATGAATAAGGTGGACATT 468
                                                                                                          760 AAGAAGAAATCTTGTTTTAAAGAGGTGGAAGTAGTALGTEVYALVYTEDYGGGTOVGY KLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    469 GAGATGCTGGAAAGGACAGAAAAGGTGGACTGGAGCAAATTCATTGCTGTGAATGGAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   580 CAGACTCTGGAGACACTAGATAAGGTAGACTACAGCAAATATGTAGCTGTAAACTTGGCA 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            460 TTCTCATACTTATCTCACACCATTCCIGAGTICACGGACAACIGCCIGATCAACATTATG 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       295 ATCTCAGAATTTGGCACGCTGGCCC1 FCCTGACCCAFGCAAGAGCAFCTTTGAACGTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            235 AAGAGCAAGITTCTACAGAGTGACACATATAAAGGCCAACAGTGCTGGAGGTAGAATTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175 TGGTTTGATGGAATGGCGTTGCTTCACCAGTTCCGAATGGAGAGGGGGCACAGTGACATAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       355 ATGTCAAGGTTTGAGC-----CACCTACTATGACTGACACACACAACGTCAACTTTGTG 408
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                                                                                                                                                                                                                                                                                                                          GATAAAGGGAGAACAAAATATGTTCTCTTTAAGATCCCTTCCTCTGTACCAGAAAAAGAA 759
                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTGCACATOCTCATTAOGACOCAGATGGGACAGCATACAACATGGGGAACAGCTATG-- 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAACTAGGATGATTATTATGCTACCAGTGAGACTAACTTCATCAGAAAAATTGATCCA 579
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                                                                                                                                                                                                                     -GGCCAAGAGGTTCTTGCTATAATATTATTCGTGTGTTCCTGCAAAAAAGAAA 635
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  1534
                                       1624 TIGGGCCGAGCCACACTTAACCTAGAAATGCATCTGGACCTGCATGGGATGTTTATACC 1682
                                                                                                                                                                                                                                                                                                                                                                                                                           1384 TATGTCTATGCAACAGAAGTCCAGTGGAGCCCCAGTTCCTACAAAGATTGCAAAACTGAAT 1443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1177 CAGGGTGATGGAGGAGTCTGGTGCTCTCCTGAAAATCTACACCAAGGAGGCTGGAAGAG 1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1231 GATGCAGAAGTAGGTTCTAATTTAGTCAAAGTTCC---AAGTTCCGGAAGTGCTGTAAAA 1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1057 TATGAGTTAAAAGGTAAAGTCTTTCCCTCGAAGATTTGTCTTGCCCTTAGATGTTAGTGTG 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1171 AACAAGCTTACCTCCATCCCAACCTGCAAGCGCTTTGTTGTTGTCTCTCTGCAGTATGACAAG 1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1111 GACAATAGCTTGTACGATATGTTTTACTTAAAAAAACTGGACAAAGAGTTTGAAGTGAACTTTAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1000 ACGAAAAAAGAAGTATCCACCAAGTTTTACACTGATGCTTTGGTGCTTTATCACCACATA 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    937 AATGUUTTUAGGACCAGGGULGTATTUTGATTUTGUGULGUUGUAGATGATGGGAAAA 996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          940 GCTTCCTGCCTTTCCTTTCATAAGGAGGATAAGACGTGGTTTCACTTTGTAGACAGAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    757 CAGCCTGTAAAGATGAAGCTGTGGAAAATAATCACTTCTAAAATCCGGGGAAAAGCCCTTT 816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   880 CAGCCATTTAAACTGGATATTGTCAAACTGGCAACTGCCTACATCCGAGGTGTGGAACTGC 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   697 ATGAAGCCTTCTTACTACCATAGCTTTGGAATGACAAAAAACTACATAATCTTTGTCGAA 756
                                                                                                                                                                                                                                                                             GATGCTGCTGAAGGAAAGAACCTCAGCCCACTGTCCTALTCTTCAGCCAGCGCTGTGAAA 1176
| CTGGGGCGAGCGGAAG LACCCG LGCAGATGCCTTACGGGTTCCATGGCACCTTTGTGCC
                                                                                                                                         GTS F0TGAG00AAATAAAG0A000TF00TA0110AT10LTGGA1G0TAAAACATT0AAAGAA | 1624
                                                                                                                                                                                        GTCCAAACAAAGGAAGIACIGCACIGGGGAGAAGACCACIGCTGGCCCTGAGAGCCCATC 1503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAGGGGGGGATTGAATTCCCTCAGATCAACTATGGCCCGATTCAATGGCAAAGGTATAGT 1296
                                                                                            -----GGGATAGAACTGCCTCGTGTCAACTATGAC---TACAATGGCAAAAAAATACAAG 1383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARCCHARACCHITACCAACTACAGAATCTCAGGAAAGCLGGAGAGGGGGCLTGATCAGGLC 1056
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                                                                                                                                                                                                                                                                                                                                                                                TTCTTCTATGGCTGCGGTT11CGACATTTGGTGGGGGGATTCTCTGTGATT---AAGGTTGAC 1353
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AAS07195 standard; cDNA; 2134 BP

AAS07195;

23-0CT-2001 (first entry)

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DNA encoding zebra-2, beta-carotene dioxygenase (Beta-diox II).

WWXEXEXXXX lycopene; beta-apocarotenal; Beta carotone dioxygenase; beta diox I; mebra 2; keta-carotene; beta-ionone; apolycopenal; seed; corn;

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CC endogenous beta-diox II. The beta-diox II specific antisense colligonucleotides derived from the DNA sequence are useful for dose colligonucleotides in relevant models of rethinoid/vitamin A deficiency cduring any stage of an organism's development. The nucleic acids are also useful as probes and as a quideline to define new PCR (polymerase chain CC reaction) primers for the cloning of substantially homologous DNA CC sequences from other sources. The nucleic acids are also useful for concession of a mount of beta-diox II nucleic acid and CC determining the presence or quantity of beta-diox II nucleic acid and CC useful for increasing or decreasing the amount of beta-diox II levels in CC a cell or tissue which can modify the level of vitamin A and other CC retinoids. Antibodies are useful for studying beta-diox II localisation, CC screening of an expression library to identify nucleic acids encoding beta-diox II or the structure of functional domains. The transgenic CC fungi, yeast, insect, animal or plant cells, seeds, issues, or whole corganisms have improved nutritional quality or physiological condition can vitamin A aldehyde and retinoic acid, beta carotene or take up beta-CC as vitamin A aldehyde and retinoic acid, beta carotene or take up beta-CC useful in the study of beta-diox II activity. Identification of constant of constant of constant and carotene/rethnoid metabolism. Vitamin A production in crops and confirmation carotene/rethnoid metabolism. Vitamin A production in crops and confirmation and constant of section and carotene/rethnoid metabolism.
     Matches 789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence represents the coding sequence of zebra-2, beta-carotene dioxygenase (Beta-diox II). Beta-diox specifically cleaves beta-carotene and lycopene to form beta-apocarotenal and beta-ionone, and apolycopenals, respectively. The DNA is useful for transforming grain seeds, e.g. corn; oil seeds, e.g. Brassica seeds, edible seeds e.g. palm, edible seeds or seeds with edible parts e.g. chick-pass; potatoes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oil seed, palm, chick pea, diagnostic, therapeutic; ribozyme; zebrafish; retinoid/vitamin A deficiency; bera-drox II- transgence; nutrition; carotene/retinoid pathway; vitamin A aldehyde; retinoic acid; crop; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            carrots, sweet potatoes, sugar beets, banana. The polypeptide is useful for diagnostic and/or therapeutle purposes and for preparing antisense ribozyme type therapeutic agents and for detecting any abnormality of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8; Page 106-109; 116pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated mouse, human, zebrafish beta-carotene dioxygenase (beta-diox II) protein that cleaves beta carotene and lycopene to yield beta-apocarotenal and beta ionone, and apolycopenals, respectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-DEC-1999; 99EP-0125895
26 MAR-2000, 2600EP 0105822
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                                                                                                         Sequence 2134 BF; 625 A; 448 C; 441 G; 620 T; 0 other,
                                                                                                                                                                                        microorganisms can be achieved by transforming the organisms or crops
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-DEC-2000; 2000WO-EF13273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GREE-) GREENOVATION PELANZENBIOTECHNOLOGIE GMFH
                            Match 8.1%;
Local Similarity 50.8%;
Conservative
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  0;
                            Score 250.8; DB 22;
Prod No 2 2e-51;
  Mismatches 712;
Indels
                                                   Length 2134;
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                            1136 TTCAATTCACTGTGTACAAACTTACCACGCCGATATGTACTGCCTCTGGAGGTGAAGGAG
                                                                            1180 ACCTCCATOCCAACCTGCAA ------GOGCTF1GT1GTGTGCCTCTGCAGTATGACAAG
                                                                                                                                  1076 GTGATTGGTGAATTCACACTGGAGAATCTACAGTCGACCGGGGAAGATCTCGACAAGTTT
                                                                                                                                                                                  1120 TTGTACGATATGTTTTACTTAAAAAAACTGGACAAAGACTTTGAAGTGAAGAACAACATT 1179
                                                                                                                                                                                                                                              1015
                                                                                                                                                                                                                                                                                              1060 AATGCTIACGAAGAAGAIGGCCACGTTCFFFILGATAICGFFGCCTACAGAGACAATAGC 1119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             896 CATAAGGTCATGTCCTGGAACCCGGAACTAGACACAATCTTTCATGTGGCAGACCGACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   836 CAGCCGATCAAGCTGGACCTGCTGAAGTTCATGCTGTACAGAATTGCTGGAAAGAGCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             940 GCTTCCTGCCTTTCCTTTTCATAAGGAGGAGGALAAGGTGGTTTCACTTTCTAGACAGAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      880 CAGCCATTTAAACTGGATATTGTTAAACTTGGCAACTGCCTACATTTTGAGGTGTGAACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     716 GACGATGATGCTGATCTGTCTGGCGCTGAAATTCTTTGCTCGATTCCTCCTCCTGCTGACCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              665 CGAAAAGGCTTCTTCTACCATATACTCAGAGTACCACC-----AGGTGAAAAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     605 ACAGCTCATCCACATTATGATCGGGAAGGAGCAACTTACAACATGGGAAACTCATATGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              545 GTGAGCCTAGAAACCAAAGAAAAGGTGGAFTGGTCCAAATTTATTGCAGTCAGIGCAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              580-CAGACTO MIAGACAMAAAAABTAAAAMTAAAATAAATAAATAATOTAAATABTAAAMTII BAAAMTII BATA-639
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                                                                                                                                                                                                                                                                                                                                                                                                       ACGAAAAAAGTAFCCACCAAGTTTTACACTGATGCTTGGTGCTTTATCACCACATA 1059
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   Sequence 1599 BP; 458 A; 354 C;
                                                               This sequence may optionally have a nucleotide extension at its 5'-region. The possible extensions are given in AAp53071-73.
                                                                                                                                                                                                                                                               New retinol binding protein receptor and homologue coding nucleic acid molecule - useful for diagnosis and treatment of retinoid linked pathological conditions, for hybridisation in stringent
                                                                                                                                                                 Claim 1; Page 21-24; 44pp; English.
                                                                                                                                                                                                                                   conditions and treating retinitis
                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAR44617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bavik CO, Eriksson U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (LUDW-) LUDWIG INST CANCER RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1613 GGACGAGCAGAAGTTCCAGTGGAACATTCCATTGGATACGGCACTCATGGACTCTTCA 1664
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Best Local Similarity 50.9
Matches 790; Conservative
                               1003 GAATTTGTTTATAATTATATATATTTAGCCAATTTACGTGAAAACTGGGAAGAGGTGAAA 1062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          700 GATAAAGGGAGAACAAAATATGITCTCIIIFAAGATCCCIIFCTCIGIACCAGAAAAAGGA 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        520 AAAACTGGGGATGATTAITATTACTACCAGTGAGACTAACTTCATCAGAAAAATTGATCCA S79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         298 ATAACAGAATTTOGCACCTGFGCTTTCCCAGAFCCCTGCAAGAATATATTTTCCCAGGTTT 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    400 GTGTCTGAGITLGGAACCALGGCTLAIGCGGAIGCAAGCAAAAAACATATTTGCCAAGGCA 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238 CACAGAAGGIICAICCGCACIGAIGCIFACGIACGGCAAFGACTGAGAAAAGGATCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 CTGTTTGALGGGCAAGCCCTCCLACAAGLTLGACTTTAAAGAAGACACATCTCACATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           280 TGGTTTGALGGCTTGGCTGCTGCACAGCTTCACGLTTAAAAATGGTGAAGTTTACTAC 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 220 GGGGTACTICICCSAAAIGGCCCAGGGALGCAAIACAAIACSGGACACTAAAIACAACCAC ±79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160 GAAGAGCATCCAGAGCCCATAAAAGCTGAGGTGCAAGGTCAGTTGCCCACTTGGTTGCAA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCT --- TGTACGATATGTTTACTTAAAAAAAACTGGACAAAAAACTHGAAGTGAACAAC 1178
                                                                                                                                                                                                ATAAATGCITACGAAGAAGATGGCCACGITGTTTTTGATATCGTTGCCTACAAATAAT 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGCCATTTAAACTGGATATTGTCAAACTGGCAACTGCCTACA---TCCGAGGTGTGAAG 936
                                                                                                                                                                 ATCAATACCTATGAAGACCATGAGTTTCTGATTGTGGATCTCTGTTGTTGGTAGAAGGATTT 1002
                                                                                                                                                                                                                                                                                                  AAAAGAAAAAGTATATCAATAATAAATACAGGACCTCTCCTTTTAACCTCTTTCATCAC
                                                                                                                                                                                                                                                                                                                                                                     AAGACGAAAAAAGAAGTATCCACCAAGTTTTACACTGATGCTTTGGTGCTTTATCACCAC 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOGGETTOTTOTTOTTTOTTTOTALANGARANGAIANGAIANGATGGTTTCACTTTGTAGACAGA 946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACACCAGTCAAAATTAATCTGTTCAAAGTTTCTTTCATCATGCAGCCCTGTGGGGGAGCCAAT 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCCAACCAAGCTACTACCACAGCTTTGGAATCACAGAAAATTATATTGTGTTCATAGAG 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTGCTCACCCCACATTGAAAATGALGGGACLGLT FACAACATTGGTAATTGCTTTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                    TACATGGATTGTTTTGAATCCAATGAAACCATGGGGGGTTTGGCTTCATATTGCTGAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45: Gaps
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                                                                                                                                                                                      11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins enoughed by the
                                                                     WPI; 2001-318749/34.
                                                                                                                                                                                                                                     29-JUL-1999;
27-AUG-1999;
                                                                                                                                                                                                                                                                                      28- 1111.-2000:
                                                                                                                                                                                                                                                                                                                       07-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                 Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cONA closse (5'-primer) SEQ ID NO-4443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH07608 standard; cDNA; 825
                                                                                                                                                     (HELI-) HELIX RES INST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1123 GACAAGGCTGACACAGGCAAGAATTTAGTCACACTCCCCAACAACTGCCACTGCCACTT 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1225 GACAAGGA FORAGAAGTAGGETETAATTI AGTETAAAGTERGCAACTER OGCAACTIGTA - 1284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106% AAAAATGCCAGAAAGGCTCCTCAGCCTGAAGCTAGGAGATACGTACTTCCTTTGAATATT 1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1174 AAGCTTACC-------CCCAPCCCAACCTGCAAGCGCTTTGGTTGTGCCTCTGCAGTAT 1224
                                                                                                                      Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGGCTGAAGTGGAGATTAACATCCCCGTCACCTTTCATGGACTGTTCAAA 1593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGAGCCACAGTTAACGTAGAAATGCATCTGGACCTGCATGGGATGTTTATA 1680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCAGGACAAAAGCCTGCTTATCTTCTGAITICIIGAAIGCCAAGGACIIGGAGTGAAGTIIGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCAA---ATAAAGCACCCTTCCTACTCATCTTGGATGCTAAAACATTCAAAGAATTGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATGGACTTGGCTTGAATCACTTTGTTCCAGACAGGCTCTGTAAGCTGAAGGTCAAAACT 1 <62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCAACAGAAGTCCAGTGGAGCCCAGTTCCTACAAAGATTGCAAAACTGAATGTCCAAACA 1452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCATTTGAGTTTCCTCAAATCAATTACCAGAAGIAIGGTGGGAAACCITACACAIAIGCA 1302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAAGAAAAAGATGGCAGCATCTATTGTCAACCTGAAATATTATGTGAAGGG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGGAAGTACTGCACTGGGGAGAAGAACCACTGCTGGGCCCTCAGAGCCCATCTTTTGTTCCCC 1512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sugiyama T,
                                                                                                                                                                                    2000JP-0118776; 2000JP-0183767.
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                                                                                                                    Nishikawa T,
                                                                                                    Wakamatsu A,
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                                                                                                                 Hayashi K,
                                                                                                    Nagai K,
                                                                                                                    Saito K,
                                                                                                      Otsuki
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Pf Claim 1: SPC 10 4443: 2537pp + CD ROM; English.

XX

Pho present invention describes primer sets for synthesising 5602

CC full-length cDNAs defined in the specification. Where a primer set or comprises: (a) an eligo-dT primer and an eligo-dT primer and an eligo-dT primer set of the complementary strand of a polynuclectide which comprises one of the 5602 nuclectide sequences defined in the specification, where the coligonuclectide comprises at least 15 nucleotides; or (b) a combination of an eligonucleotide which comprises a 5'-end complementary strand of a polynucleotide which comprises a 5'-end complementary strand of a polynucleotide which comprises a 5'-end complementary and individual electide comprises a 3'-end sequence, where the combination of the 5'-end sequence/3'-end sequence is selected from those defined in gene therapy. The primers sets can be used in antisense therapy and complementary full-length cDNAs. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the complementary in the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length day specialised methods AAH3465 to AAH3482 and AAH3482 conditions and AAH3467 to AAH3482 conditions.

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Sequence 825 BP: 238 A; 159 C: 216 G: 204 T: 8 other:
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400 GFRETERARITERGACIATRARITERAN INGRADIO ATRICAAAAAACATATITG-----CC 453

AGGAGG AAGT FETI ACAGAG EGATACA LATAAGAG CAACAG LG TIAAAAAC CGAA LIGI E

423

514 ATTATGAAAACTGGGGATGATTATTATGCTACCAGTGAGACTAACTTCATCAGAAAAATT 573

QY 633 CTTG 636

) b 664 ATGG 667

RESULT 13
AAQ53074
11 AAQ5307

i AA@11074 stabdard, cFWA, 1265 BP.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.4%; Score 104 6; DR 14; Length 1265; Best Local Similarity 47.9%; Pred. No. 1.6e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New retinol binding protein receptor and homologue coding nucleic acid molecule - useful for diagnosis and treatment of retinoid linked pathological conditions, for hybridisation in stringent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1265 BF; 379 A, 310 C, 210 G, 363 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence may optionally have a nucleotide extension at its 5'-region. The possible extensions are given in AAQ53071-73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 5; Page 26; 44pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         conditions and treating retinitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAR44618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1993-386570/48.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-MAY-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-JUN-1994 (first entry)
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876 AGAGCAGCCATTTAAACTGGATATTGTCAAACTGGCAACTGCCTACATCC---GAGGTGT 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                           816 CCTGCTCCAACCAAGCIACIACCACAGCTITGGAATCACAGAAAATTATATTGTGTTCAT 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             636 GGCAACTTCTCACCCACACTATGACAGTGCTGGAAATATTCTCAACATGGGTACTTCAAT 695
                                                                                                      353 CAAAAAAACCAAAAACTACCTCAATAATAAATACACAACTTCTCCTTCCAACCTCTTCCA 412
                                                                                                                                                      993 CASAAAGACGAAAAAAGAAGTAICCASTAAGIIITACACIGAIGCTTFGGTGCTTTAICA 1952
                                                                                                                                                                                                        293 CAACTACATGGATTOTTTTGAGTOCAATGAAAGCATGAGNATTIGGGTIFATATAGTFGATAK
                                                                                                                                                                                                                                                          933 GAACIGGGCTTCCTGCCTTTCCTTTCATAAGGAGATAAGACGTGGTTTCACTTTGTAGA 992
                                                                                                                                                                                                                                                                                                            233 GGAGACACCAGTCAAAAITAACCICITCAACTTCCITTTTTCATCCAGICITTEGGGAGC 192
                                                                                                                                                                                                                                                                                                                                                                                                              173 CCGAFTCAACCCATCTTACGITCATAGTFFTGGTCTGACTCCCAACTATATCGTTTTTGT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 AGCAGACAAGGAAGATCGAATAAGGAAGTGAGAGATGGTNGTAGAATTGGGGTGGAGIGA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               756 AGAAAAGAAGAAATCTTGTTTTAAACACCTGGAAGTAGTATGCTCCATCCCTTCTCGCTC 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              696 TOTTGATAAAGGGAGAACAAAATATGTTCTCTTTAAGATCCCTTCCTCTGTACCACAAAA 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 TGGAAAAAATTTTTCAATTGCCTACAACATTGTAAAQATGCC------ACCACTGCA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GGCCACTGCTCACCCCCACATTGAAAATGATGGAACCGTTTACAATATTCGTAATTGCTT 61
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Mismatches 521; Indels 39;
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     RESULT 14

ABL29861

ID ABL29

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PR 23-MA

PR 2
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New isolated nucleic acid detection reagent for detecting 1900 or
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                                                                                                    Venter JC,
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11-JUL-2000; 2000US-0614150.
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Drosophila melanogaster genomic polynucleotide SEQ ID NO 41056.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful in developmental biology and in elucidating cell signalling cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABLIG171), expressed DNA sequences (ABLIG1840-ABLIG175) and the encoded proteins (ABB57237-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        capable of detecting 1000 or more genes from Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEv ID NO 41056; zlpp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genes from Drosophila and for elucidating cell signalling and cell-cell
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                                                                                                                                 ---TTCGAGGATGCTCATGTGGTGGCCACACIGCCGIGCCGCTGGAAACTGCATCCCGGT
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                                                                                                                                                                                                                                                                                                         CATGITCITCCCAGIGGCACIGICIACAACCTGGGCACCACAAT--
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                                                                                    TACTACCACAGCTTTGGAATCACAGAAATTATATTGTGTTCATAGAGCAGCCALTTAAA
                                                                                                                                                                                                                     ACCAGATCTGGACCGGCATACACTATACTCAGTTTCCCCGCACGGCGAGCAGATG-----
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                                                                                                                                        The sequence represents the coding sequence of Drosophila beta-carotene dioxygenase (Beta-diox I). Beta-diox specifically cleaves beta-carotene and lycopene to form beta-apocarotenal and beta-ionone, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oul seed; palm, chick-pea, diagnostic; therapeutic, ribozyme; retinoid/vitamin A deficiency; beta-diox II; transgenic; nutrition; carotene/retinoid pathway, vitamin A aldehyde; retinoic acid; crop;
                                                                                                                                                                                                   Disclosure; Fig 6; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                  27-DEC-2000; 2000WO-EF13273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W0200148163-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding Prosophila beta-carotone dioxygenase (Bota-diox I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-001-2001
                                                                                                                                                                                                                              beta apocarotenal and beta-ionone,
                                                                                                                                                                                                                                                                                                                                                             (GPEE-) GREENOVATION PELANZENRICTECHNOLOGIE GMBH
                                                                                                                                                                                                                                                                                                                                                                                        20-MAR-2000; 2000EP-0105822
                                                                                                                                                                                                                                                                                                                                                                                                    24-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lycopene; beta apocarotenal;
                                                                                                                                                                                                                                           Novel isolated mouse, human, zebrafish beta-carotene dioxygenase (beta diox li) protein that cleaves beta carotene and lycopene to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1145 CGGGATGGCCACGTGGTGGTGGACATTTGCAGCTACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1072 GAAGATGGCCACGTTGTTTTTGATATCGTTGGCTACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             968 GITTOSCITACOSASTATATCAAASCOCAGCTAGGTGGACACAACITATCGGCGTCTCTC 1027
                                                                                                                                                                                                                                                                                       AAU04291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGCAGACCTACGAAT---CGGAAGCCTTCTTCTACCTGCACATCATCAACTGCTTTGAA 1144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTATCCACCAAGTTTTACACTGATGCTTTGGTGCTTTATCACCACATAAATGCTTACGAA 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGTG3TFTGAA33ATG3ACC3ACC3ACACTATFTGAGAGGTTATAGAGAGGGTTTGGGGGAAAGTG 1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             melanogaster
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                                                                                                                                                                                                                                                                                                                                Vogt
                                                                                                                                                                                                                                                                                                                                                                                                    99EP-0125895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "Beta-carotene dioxygenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualitiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .1863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 beta ionone; apolycopenal
                                                                                                                                                                                                                            and apolycopenals, respectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (beta-diox I)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  grain seed,
                                                                                                                                                                                                                                          yield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COID;
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upolycopenals, respectively. The DNA is useful for transforming grain seeds, e.g. corn; oil seeds, e.g. Brassica seeds; edible seeds e.g. palm; edible seeds or seeds with edible parts e.g. chick-peas; potatoes, carrots, sweet potatoes, sugar beets, banana. The polypeptide is useful for diagnostic and/or therapeutic purposes and for preparing antisense or ribozyme type therapeutic agents and for detecting any abnormality of endogenous beta-diox II. The beta-diox II specific antisense oligonucleotides derived from the DNA sequence are useful for dose response studies in relevant models of rethnoid/vitamin A deficiency during any stage of an organism's development. The nucleic acids are also

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Matches 444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organisms have improved nutritional quality or physiological condition and accumulate important metabolites of cartoteme/fethnoid pathways such as vitamin A aldebyde and retinoic acid, beta-carotene or take up beta-carotene from the medium. Expression systems encoding beta-diox II are useful in the study of beta-diox II activity. Identification of cDNAs encoding beta-diox I and II allows the physiological characterisation of mammalian carotene/retinoid metabolism. Vitamin A production in crops and microorganisms can be achieved by transforming the organisms or crops
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  determining presence and amount of beta-diox II. The polypeptide is also useful for increasing or decreasing the amount of beta-diox II levels in a cell or tissue which can modify the level of vitamin A and other retinoids. Antibodies are useful for studying beta-diox II localisation, screening of an expression library to identify nucleic acids encoding beta-diox II or the structure of functional domains. The transgenic fundi, yeast, insect, animal or plant cells, seeds, lissues, or whole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful as probes and as a guideline to define new PCF (polymerase chain reaction) primers for the cloning of substantially homologous DNA sequences from other sources. The nucleic acids are also useful for determining the presence or quantity of beta-diox II nucleic acid and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2037 BF, 492 A; 521 C, 531 G, 493 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      with the cDNAs.
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532 GATTATTATGCTACCAGTGAGACTAACTTCATCAGAAAAAFTGATCCACAGAGCTCTGGAG 591
                                                                                                                                      517 CAGTATTACACATTTACGGAGACGCCTTTTATGCATAGAATAAATCCCTGGACTTTGGCC 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          472 TCTCACACCATTCCTGAGTTCACGGACAACTGCCTGATCAACATTATGAAAACTGGGGAT 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       412 GGAACCATGGCTTAICCGGAICCATGCAAAAACATATTTGCCAAGGCATTCTCATACTTA 471
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                                                                                                                                                                                                                        772 TGTTTTAAACACCTGGAAGTAGTATGCTCCATCCCTTCTFGCTGCTGCTGCTGCACCAAGC 831
                                                                                                                                                                                                                                                                                                                        682 ACCAGATCTGGACCGGCATACACTATACTCAGTTTCCCGGCACGGCGAGCAGATG-----
                                                                                                                                                                                                                                                                                                                                                                                                              652 CACTATGACAGTGCTGGAAATATTCTCAACATGGGTACTTCAATTGTTGATAAAGGGAGA 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  592 ACACTAGATAAGGTAGACTACAGCAAATATGTAGCTGTAAACTTGGCAACTTCTCACCCA 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    460 TTTCGACCGGATAGTG---GAACGGATAACTCGATGATTTCCATATATCCTTTCGGGGGAT 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     403 GGCACAGCTGCTGTTCCGGATCCCTGTCACTCGATCTT---CGATAGATTTGCGGCCATT 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  343 GTGGACACGGAAACACTGCGAAAGAATCGCTCTGCCCAGCGGATTGTGGTCACGGAGTTT 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232 CGAANTCGCCCAGGGAFGCACACAAFAGGGGACACTAAATACAACCACTGGFFFGAFGGC 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    352 CTCCGAAGTGACACATACAACTGCAATATAGAAGCAAACCGAATCGTGGTGTCTGAGTTT 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    283 TCCGCCCTGCTGCACCGATTTGCCATTCGGAATGGACGCGTCACCTACCAGAATCGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223 CGCAATGGACCCGGCAGCTGGAAGGFGGGCGACATGAGGTTGGGCCATCTGTTGGACTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCGAAGCACGAATCTGCACCACCGACTTCGTGGGCGTGGTGAACCACACATCGCATCCG 636
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1030 CGGGATGGCCACGTGGTGGTGGACAFITGCAGCIACAG 1067
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                                               1072 GAAGATGGCCACGTTGTTTTTGATATOGTTTGCCTACAG 1109
                                                                                                   973 GTGCAGACCTACGAAT----CGGAAGCCTTCTTCTACCTGCACATCATCAACTGCTTTGAA 1029
                                                                                                                                                                                                          913 AAGTGGTTCGAGGACCGACCGACACIAIIICACCITAIAGAIGGGGTTICCGGCAAACIG 972
                                                                                                                                                                                                                                                            853 GITTCGCTTACGGAGTATATCAAAGCCCAGCTAGGTGGACAGAATTTATCGGCGTGTCTC 912
                                                                                                                                                                                                                                                                                                                                                                  892 CTGGATATTGTCAAACTGGCAACTGCCTACATCCGACGTGTGAACTGAGCTGCGCCTTCCTGCCTT 951
                                                                                                                                                                                                                                                                                                                                                                                                                       793 TATATGCACACCTTCGGCTTAACGALCACTACTACTGTGALTGTGGAGCAGCCGCTTGTCC 852
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Search completed: July 15, 2003, 20:15:30 Job time: $649 \ \text{secs}$

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OM protein - protein search, using sw model
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973.470 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Canine RPE65. Can	AAB73955	22	533	37.9	1071	10
Human-2, beta-caro	AAU04294	ر ، د ،	7.7.	30 0	1102 5	9
Buman protein sequ	AABGRASH	۲.	7 14	44.0	1102 5	8
Mouse-2, beta-caro	AAU04292	() ()	5.35	39 4	1112.5	7
Human RECAF polype	AAR68872	(1 (1	579	д Б	1116 5	6
<pre>"cbra-2, bcta-carc</pre>	AAU04293	۲.1 د ا	549	40 4	1142 5	5
Amino acid sequenc	AAC62840	C1	516	60.7	1715	4
Human protein sequ	AAR93108	ر د	547	74.6	2107	ω
Beta, Beta caroten	AAY97314	21	506	96.3	2721	ı
Rota, Bota-maroton	AAY97 +11	-1	£	loa ŝ	5,48,4	1
bescription	ID		Length	Query Match Length DE	410.0S	Result No

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133	. j. j.	207	216.5	0.77	131.5	233.5	233.5	[년 [년 년 1년	233.5	237.5	139.5	239.5	247	260	260	263	263	276	715	307	307	307	310	311	373.5	5.20	541	576.5	840 =	840.5	040.T	1014.5	1070
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ABG14465	AAE72307	AAF04792	APC14467	AAFO4 / B7	AAB72303	AAB72306	AAE04783	AAG 31333	AAC31334	ABB91182	AAB72309	AAE04788	ABG14652	ABR92311	AAE04784	АВН92416	AAE04785	AARTITAAA	AAED4789	AAG13115	AAG13116	AAC13117	AAE04785	AAE04790	AAB73956	AAE12065	AAE12066	AAR44618	AACE: 841	AAM94291	APB71747	AAY97315	AAP44617
Novel human diagno	- 2	Arabidopsis thalia	Novel human diagno	Vigna unquiculata	Suntlewer neemanth	Neoxanthin cleavag	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	Herbicidally activ	Neckanthin cleavag	<pre>2ca mays neoxanthi</pre>	Novel human diagno	Herbicidally activ	Arabidopsis thalia	Herbicidally activ	Arabidopsis thalia	Neoxanthin clea∵ag	Lycopersions escul	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia		Arabidopsis thalia	Prog	Arabidopsis thalia	Arabidopsis thalia	Human retinol bind	Arine arid sequenc	Prosophill beta-ca	Errescphila melanog	Beta, Beta caroten	Human retinol bind

ALIGNMENTS

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RESULT 1
AAY97311
Forta, beta-carotype: 15,15-dimxyamnase, vitamin A. beta-carotene; transformation, truit, vegetable, developmental disorder; ophthalmological disorder; antibody; detection; quantification;
        N-PSDB; AAA53888
                   WPI; 2000-551036/51
                                                                                                              17-PEH-2000; 2000EP-0102289
                                                                                                                                                        EP1031627-A1
                                                                                                                                                                          Gallus gallus.
                                                                                                                                                                                                                                                                     03.JAN-2001 (first optry)
                                                                                                                                                                                                                                                                                            AAY97311;
                                                                                                                                                                                                                                                                                                                AAY97311 standard; Protein; 526 AA.
                                                 Rachmans H,
                                                                                          22-FEB-1999;
                                                                                                                                   30-AUG-2000.
                                                                                                                                                                                               treatment; therapy.
                                                                                                                                                                                                                                                  Beta, Beta-carotene-15,15-dioxygenase
                                                                     (HOFF ) HOFFMANN LA POCHE & CO AG F
                                                 Progger P,
                                                                                           99EP-0103382
                                                  Priedlein AM,
                                                  Wirtz CM,
                                                  Wio-jjg∈n W,
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AAY97 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 526; Conservative
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03-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heta, beta-carotene-15,15'-dioxygenase (bCOD) is used for enzymatic conversion of beta-carotene to vitamin A and for raising specific antibodies. Nucleotides encoding all or part of bCDD are useful as primers or probes for specific amplification and/or detection of the gene that encodes bCOD, for isolation of related sequences in other organisms, for determining bCDD levels in humans (to identify
                                                                AAY97314 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       subjects requiring vitamin A supplementation) and for detecting mutations in the bCOD gene. The nucleatide enougher bCOD may also be used to transform cells, particularly plant cells, to increase their vitamin A contents (especially in truits and vegetables) and in gene therapy of subjects who have mutated or deleted forms of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heta, beta-carotene 15,15′-dioxygenase protein, nucleic acids and antibodies, useful for production of vitamin A from carotene and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          against bCOD are used for detection/quantification of bCOD in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bCOD gene and thus low vitamin A levels and susceptibility to developmental or ophthalmological disorders. Antibodies raised
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                                                                                                                                           481 PNKAPFILILDAKTEKELGRATVNVEMHLDLHGMEIPQNDLGAETE 526
                                                                                                                                                                           481 PNKAPFILII.DAKTFKELGRATVNVEMHI.DI.HGMFTPQNDI.GAETE 526
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                                                                                                                                                                                                                                                                                                     361 PLQYDKDAEVOSNLVKLPTSATAVKEKDGSTYCQPEILCEGIELPRVNYDYNGKKYKYVY 420
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                                                                                                                                                                                                                                                                       ATEVQWSPVPTKIAKLNVQTKEVLHWGEDHCWPSEPIFVPSPDAREEDEGVVIJCVVVSE 480
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Pred. No. 2.2e-247;
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subjects requiring vitamin A supplementation) and for detecting mutations in the bCOD gene. The nucleotide encoding bCOD may also be used to transform cells, particularly plant cells, to increase their vitamin A contents (especially in truits and veopriables) and in gene therapy of subjects who have mutated at detect from bCOD gene and thus low vitamin A levels and susceptibility to developmental or obthalmological discoders. Antibodies raised against bCOD are used for detection/quantification of bCOD in
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310 NAYEEDGHVVFUIVAYKUNSLYEMFYLKKLUKDFEVNNKLISIFICKKFVVFLQYDKDAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 KTGDDYYATSETNELKKICFOTLETIDKVDYSKYVAVNIATSHPHYDSAGNILNMSTETV TBS
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                                                                                     QPEKLDIVKLATAYIRGVNWASCLSEHKEDKTWEHFVDPKTKKEVSTKFYTDALVLYHHI
                                                                                                                                                                     QPEKLDIVKLATAY I KGVNWASCLSTHKEDKIWTHF VDRKIKKEVS I KFYTDALVLYHHI
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of an oligonuclective comprising a sequence complementary to the complementary straid of a polynucleotide which comprises a 5'-end sequence and an aligonucle-didevice comprises a 3'-end sequence, where the oligonucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the defenction and/or blaguesis of the abnormality of the primits encount the full-length cDNAs. The primers are also useful for the
                                                                                                                                                                                                           The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynoclasside which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of specification comprises at least 15 nucleotides; or (b) a combination
                                                                                                                                                                                                                                                                                                                                                                                       Primer sets for synthesizing polynucleorides, particularly the 5502 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
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02-MAY-2000; 2000JP-0183767
09-TUN-2000; 2000JP-0241899
                                                                                                                                                                                                                                                                                                                                                   Claim 8; SEQ ID 11972; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUL·1999;
27-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lsogai T,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LDAKTFKELGRATVNVEMHLDLHGMF 515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sogai T, Nishikawa T, Hayashi K,
Sugiyama T, Wakamatsu A, Nacai
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99JP-0300253
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481 TDPQKLPFLLILDAKSFTELARASVDVDMHMDLHGLFITDMD 522
                                         479 SEPNKAPELLILDAKTEKELGPATVNVEMHLDLIGMELPOND 520
                                                                                                                                    419 VYATEV@WSTVFTKTAKLNV@TKEVLHWGEEHIWFSEFIFVFSF@ASEEEEEGVVLIIOVVV
                                                                                                                                                                                   361 VFLHVDKNAEVGINLIKVASITATALKEEDGQVYCQPEFLYEGLELFRVNYAHNGKQYRY
                                                                                                                                                                                                                                                                                                                        300 TDALVLYHHINAYEEDGHVVFDIVAYRDNSLYDYFYLKKLDKDFEVNNKLTSIPTCKRFV
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                                                                                                                                                                                                                                                                                                                                                                                                                   240 ITENYIVELEOPEKLDIVKLATAYIFGVNWASCLSFHKEDKIWEHFVDEKTKKEVSTKFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 TENMGESTADEGESKAATEKIESSADE - KEKKKSCEKHTEAACSTESESTIDESAAKEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 TDNCLINIMKTGDDYYATSETNFIRKIDPQTLETLDKVDYSKYVAVNLATSHPHYDSAGN
                                                                                                                                                                                                                                360 VPLQYDKDAEVGSNLVKL-PTSATAVKEKDGSIYCQPEILCEGIELPKVNYDYNGKKYKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 367;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 METIFNRNKEEHPEPIKAEVQGQLPIWLQGVLLKNGPGMHTIGDIKYNHWFDGLALLHSF
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                                                                                           VFATGVQWSPTPTKIIKYDILTKSSLKWREDDCWPAEPLFVPAPGAKDEFRØVILSAIVS
                                                                                                                                                                                                                                                                            TGAMVVEHHVNAYEEDGCIVEDVIAYEDNSLYGLEYLANLNGDEKENSELTSVETLEREA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIPDGEVYYRSKYLPSDTYNTNIEANPIVVSEFGTMAYPDDGKNIESKAFSYLSHTIDDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TEKNGEVYYRSKYLRSDTYNCNTEANRIVVSEEGTMAYPDPCKNTEAKAESYLSHTTDEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TONGLINIMKOGEDEYATSETNYIRKINEQTLETLEKVDYRKYVAVNLATSHPHYDEAGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            547 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74.6%; Score 2107; DB 22; 70.3%; Pred. No. 3.3e-182; ative 96; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 547;
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Beta carytene diexygenase; beta diex, beta caretene; vitamin A aldehyde;

transgenie plant Danio rerio. Wuzuel48162-A2.

20-MAR-2000; 200049-0105822

24 - PEC - 1999;

2685C10-1366

22-PEC-2000; 2000WO-EP13144

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    up beta-carotene from the medium. Expression systems encoding beta-diox are useful in the study of beta-diox activity. Identification of conas encoding bota-diox allows the physiological characterization of mammalian vitamin A metabolism. Vitamin A production in crops and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plants The transpenic plants have improved nutritional quality or physical equalition and accumulate vitamin A aldehyde and can take
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a beta-carotene dioxygenase (beta-diox) polypeptide. Beta-diox specifically cleaves beta-carotene to form vitamin A aldehyde. Beta-diox is is useful for producing transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           microorganisms can be achieved by transforming the organisms or crops
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Page 86-87; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dioxygenase (beta-diox) protein that cleaves beta carotene to form vitamin A aldehyde, and polynucleotides encoding them usoful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               with the cDNAs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               producing transgenic bacteria, fungi, plants expressing the polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                         415 SYMCCVDESPVATRIVKFDADTKQQIEWKGDDGFASEPVFIPRPGAVDEDDGVVLTVIIN 474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      310;
NKPLQGGFLLVLDAKSFKEIARACLDVEIHMDMHGYFIP 513
                                            SEPNKAPFLLILDAKTFKELGRATVNVEMHLDLHGMFIP 517
                                                                                                                                   VYATEVQWSFVPTKIAKLNVQTKEVLHWGEDHCWPSEPIFVPSPDAREEDEGVVLTCVVV 478
                                                                                                                                                                                       FPL--SDQGETGEDLVKLKYTTASAVKEKDGKIMCQGEVLCEGVELPRINYNFNGKKYRY
                                                                                                                                                                                                                                  VPLQYDKDAEVGSNLVKLP-TSATAVKEKDGSIYCQPEILCEGIELPFVNYDYNGKKYKY 418
                                                                                                                                                                                                                                                                                                                           TDALVLYHHINAYEEDGHVVFDIVAYRDNSLYDMFYLKKLDKDFEVNNKLTSIPTCKRFV
                                                                                                                                                                                                                                                                                                                                                                                                                       ITENYIVE IEQPEKLDIVKLATAY IRGVNWASCLSEHKEDKTWEHEVDRKTKKEVSTKFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYSMGTCTAEKGKTKYMLEKVPGCSPPDGSPP---LKSAEAVCTLPCRSLLTPSYYHSFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ILNMGTSIVDKGRTKYVLFKIP-SSVPEKEKKKSCFKHLEVVCSIPSRSLLQPSYYHSFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TDNCGNNIIKYGNDFHATSETNYIRKIDPVTLETQEKIDYLKYLPVSIVASHTHYDKEGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TONCLINIMKTGDDYYATSETNFIRKIDPQTLETLDKVDYSKYVAVNLAISHPHYDSAGN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TFKNGEVYYRSKYLRSDTYNCNIEANRIVVSEFGTMAYPDPCKNIFAKAFSYLSHTIPEF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  \tt METIFNRNKEEHPEPIKAEVQGQLPTWLQGYLLRNGPGMHTIGDTKYNHWFDGLALLHSF
                                                                                                                                                                                                                                                                                 TDAMTYYHQVNAFEDIX;HVVFDVIAYDDNNLYEFFYLNKI.KFTMGATN-LYCKPKFTPFV
                                                                                                                                                                                                                                                                                                                                                                          MTDNYFIFIEQFLKLDILKMATAYLEEVSWASCMKEHPEDSTLIHLIDRNTKKEVATKEY 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MQYDYGKNKEEHPEPIKTEVKGSIPEWVQGTLIKNGPGMESVGETTYNHWEDGMALLHSE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           516 AA;
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AAU04293

AAU04293 standard; Protein; 549 AA

Query Match

40.4%

Score 1142.5,

11.

Sequence

549 AA

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organisms have improved nutritional quality of physiological condition and accomplate important melabolites of cardenoted involviment pathways such as vitamin A alcohyde and retirols acid, bota-cardeno it ake up hota cardeno from the medium. Expression systems encoding bota-diox II are useful in the study of beta-diox II accivity. Identification of clNAs encoding bora-diox I and II allows the physiological characteristation of mammalian carotene/retiroid metabolism. Vitamin A production in crops and
                                                                                                                                                                                                                                                      determining the presence or quantity of beta-diox II nucleic acid and determining presence and amount of beta-diox II. The polypoptide is also useful for increasing or decreasing the amount of beta-diox II levels in a cell or tissue which can modify the level of vitamin A and other a cell or tissue which can modify the level of vitamin A and other retinoids. Antibodies are useful for studying beta-diox II localisation, screening of an expression library to identify nucleic acids encoding beta-diox II or the structure of functional domains. The transquaic
                                                                                                                                                                                                                                                                                                                                                                                                                                   response studies in relevant models of retinoid/vitamin A delicioncy during any stage of an organism's development. The nucleic acids are also useful as probes and as a quideline to define new PCR (polymerase chain reaction) primers for the cloning of substantially homologous DNA sequences from other sources. The nucleic acids are also useful for sequences from other sources.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              edible seeds or seeds with edible parts e.g. chick peas; potators, carrots, sweet potatoes, sugar beets, banana. The polypeptide is useful for diagnostic and/or therapeutic purposes and for preparing antisense or ribozyme type therapeutic agents and for detecting any absorbability of endogenous beta-diox II. The beta-diox II specific antisense of oligonucleotides derived from the DNA sequence are useful for descentions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          apolycopenals, respectively. The DNA is useful for transforming grain seeds, e.g. corn; oil seeds, e.g. Brassica seeds, edible seeds e.g. palm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence represents the amino acid sequence of zebra 2, beta-carotene dioxygenase (Beta-diox II). Beta-diox specifically cleaves beta-carotene and lycopene to form beta-apocarotenal and beta-lonone, and
                        microorganisms can be achieved by transforming the organisms or crops
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lycopene; beta-apodarotenal; beta-ionome; apolycopenal; grain seed; cornoll seed; palm, chick-pea, diagnostic, therapeutic, ribozyme, schrafish; retinoid/vitamin A deficiency; beta-diox II; transgenic; nuturition; carotene/retinoid pathway; vitamin A aldebyde; retinoic acid; crop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Fig 14; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated mouse, human, zebrafish beta-carotene dioxygenase (beta-diox II) protein that cleaves beta carotene and lycopene to yield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSUB; AAS07195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GREE-) GREENOVATION PFLANZENBIOTECHNOLOGIE GMBH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 DEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W0100148163-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zebra-2, beta-carotene dioxygenase (Beta-diox II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAUC4293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-425657/45
                                                                                                                                                                                                                                yeast, insect, animal or plant cells, seeds, tissues, or whole
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5685770-4388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nootropic, neuroprotective; anticanvolsant; antipatkinsonian; anti-HIV; antidabetic; immunostimulast, immunostimulast, immunostipotestativ; actionalistic thyromimetic; antibyodi, immunostippressive; nephrotropic, antiquout thyromimetic; cytostatic; antibacterial; virucide; fungicide, protromacide, antiarteriosclerotic; hepatotropic, gene therapy, infection; cancer.
                                                                                                                                                                                                                             21-JUL-1999;
07-OCT-1999;
    Baughn MP,
                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W0200107612-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human RECAP polypeptide, SEQ ID No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB68872 standard; Protein; 579
                                Au-Young J,
                                                                                                                (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                              21-JUL-2000; 2000WO-US20035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; RECAP; recriptors and associated proteins; objective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  310 NAYEEDGHVVFDIVAYRDNSLYDMFYLKKL-----DKDFEVNNKLTSIPTCKKFVVPLQY 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250 CEFKLEIVKLATAYIRGVNWASCLSFHKEEKTWEHFVEEKTKKEVSIKEYILALVLYHHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    213 PROFEYHIL KVEVG - EKODODARLSGAEIL SIPAAOPEKESYYHSEVMSENYIVEIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153 KYKGDFYVSTETNFMRKIDPVSLETKEKVDWSKFIAVSAATAHPHYDREGATYNMGNSYG 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              365 DKDAEVGSNLYKLP-TSATAVKEKIRJ-----STYCQPEILCEGIELPRVNY-DYNGKKY 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 KTGDDYYATSETNEIFKIDPÖLLETLÖKVDYSKYVAVNLATSHPHYDSAGNILNMGTSIV 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 SSRFIQSDSYVQNSEKNRIVVSEFGTI ATPDPPCKNIFAPFFSRFQ--IPKTTDNAGVNFV 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 RSKYLRSDTYNCNIEANRIVVSEFGTMAYPDPCKNIFAKAFSYLSHTIPEFTDNCLINIM 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 EEHPEPIKAEVQGQLPTWLQGVLLKNGFGMHTIGDIKYNHWFDGLALLHSFTFKNGEVYY 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VVSEPNKAPFLLILDAKTFKELGRATVNVEMHLDLHGMF 515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KYVYATEVQWSFVF1KIAKLNVQTKEVLHWGEDHCWFSEFIFYFSFDAREEDEGVVLTCV 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEDEPNDÖNLINLPYTTASAVKTÖTGVFLYHELLYNLDLLQYGGLEFPQINYANYNARPY 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EEIPDPITTLIKGQIPSWINGSFLRNGFGKFEFGESKETHWFDGMALMHREN1KDGQVTY 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITPREKKSSFLLVLDAKTFTELGRAEVPVDIPYGTHGLF 545
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    Lu DAM,
                                    Bandman O,
                                                                                                                                                                                                                                 99US-0145232
99US-0158578
                                                                                                                                                                                         9908-0165192
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    Hillman JL,
                                Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1114
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    Patterson
                                    Yue H, Azimzai Y,
Lal P;
                                    Burford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   t .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disinders such as AIRS, Tiberrae's syndrome, ordined immunicate price programs (STI). Chadrak Higashi syndrome, Onshing's disease, Addison's disease, autoimmune thyroiditis, Cichn's disease, disease, autoimmune thyroiditis, Cichn's disease, disease, syndrome, gout, Grave's diseases, Hashimoto's thyroiditis, Siogren's syndrome, Werner's syndrome, viral, bacterial, forgal, parasitie, parasitie, and halminthic infections; and cell proliferation disorders such as afteriosclerosis, atheroscietosis, cirrhosis, hepatitis and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease, dementia, Parkinson's disease, Downs's syndrome, amyotrophic lateral solerosis, multiple solerosis, bacterial and viral meningitis, con corrected and viral solerosis, multiple solerosis, bacterial and viral seniorists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is a human PECAP (receptors and associated proteins) polypeptide. PECAP polynucleatides and polypeptides are useful in the diagnosis, treatment and prevention of neurological disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel receptors and associated proteins for diagnosis and treatment of neurological disorders, immunological disorders including autoimmune/inflammatory disorders and cell proliferative disorders such as cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       such as stroke, Alzheimer's disease, Pick's disease, Huntington's
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDR; AAF58596
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                                                                                        474 TCVVVSEPNKAPFLLILDAKTFKELGRATVNVEMHLDLIGMFIP 517
                                                                                                                                                                                                                                                                          414 KKYKYVYATEVOMSPVPTKIAKENVOTKEVIHWGETHOWESEPIEVPSPDARFEDEGVVL
                                                                                                                                                                                                                                                                                                                                                                       416 NVSLNAPEGDNLSPLSYTSASAVKQADGTIWCSHENLHQEDLEKEGGIEFPQIYYEKESG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                363 QYDKDAEVGSNLVKLP-TSATAVKEKDGSIYCQPEILCE------GIELPRVNYD-YNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      308 HINAYEFFGHVVFDIVAYPONSIYDMFYLKKLDK···· DFFVNNKLTSIDTCKREVVPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 EEHPEPIKAEVOGOLPTWLOGVLLRNGPGMHTIGDTKYNHWFDGLALLHSFTFKNGEVYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 EEAPPGISARVWGHEPKWLNGSILRIGPGKEEFGKDKYNHWEDGMALLHGERMAKGIVTY 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QTNAFEDQ@ZYTTDL/ZS@FingRelleVY@L@NL#KAGEGLDQVHNSAAKSEP---RREVLPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IEQPERMNEWRIAISKIEGKAESOGISWEDGINTEEBVV-KEIOGITPGETOFFPEVIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HA IA IMULA ELLA EN ANTA EL MARTA EN TRA PORTA P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IVDKGRTKYVLFKIESSVEEKEKKKSGEKHLEVVGSIESKSLLOESYYHSEGITENYIVE 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YVRYKGDYYLCTETNEMNKVDIETLEKTEKVDWSKFIAVNGATAHHHYDEDGIAYNMONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMKTGDDYYATSETNFIRKIDPQTLETLDKVDYSKYVAVNLATSHPHYDSAGNILNMGTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RSKFLOSDTYKANSAKNRIVISEFGTLALPDPCKNVFERFMSPFELPGKAAAMTONTNVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RSKYLRSDTYNCNIEANRIVVSEFGTMAYPDPCKNIFAKAFS--YLSHTIPEFTDNCLIN
                                                                                                                                                                                 KKYHFFYGCGFR-HLVGDSLIKVDVVNKTLKVWREDGFYFSEPVFVPAPGINEEDGGVIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                579 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23;
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RESULT 7

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corresponse studies in relevant models of rethnoid/vitamin A deficiency (contring any stage of an organism's development. The nucleic acids are also useful as probes and as a guideline to define new PCR (polymerase chain consecution) primers for the cloning of substantially homologous DNA (context of the presence or quantity of beta-diox II nucleic acid and context of the presence or quantity of beta-diox II nucleic acid and context of the presence and amount of beta-diox II. The polypeptide is also useful for increasing or decreasing the amount of beta-diox II levels in context of the context of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              carrots, sweet potatoes, sugar beets, banana. The polypeptide is useful for diagnostic and/or therapeutic purposes and for preparing antisense or riboxyme type therapeutic agents and for detecting any abnormality of endogenous beta-diox II. The beta-diox II specific antisense oligonucleotides derived from the DNA sequence are useful for dose oligonucleotides derived from the DNA sequence are useful for dose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence represents the amino acid sequence of mouse 2, beta-carotene dioxygenase (Beta-diox II). Beta-diox specifically cleaves beta-carotene and lycopene to form beta-appearotenal and beta-ionone, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lycopene, beta apocaretenal; beta ionone, apolycopenal; grain seed; coin; oil seed; palm; chick-pea; diagnostic; therapeutic; ribozyme; retinoid/vitamin A deficiency; beta-diox II; transgenic; nutrition;
                                                       with the cDNAs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            apolycopenals, respectively. The DNA is useful for transforming grain seeds, e.g. corn; oil seeds, e.g. Brassica seeds; edible seeds e.g. palm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Fig 14; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      edible seeds or seeds with edible parts e.g. chick-peas; potatoes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        beta-apocarotenal and beta-ionone, and apolycopenals, respectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated mouse, human, zebratish beta-carotene dioxygenase (beta-diox II) protein that cleaves beta carotene and lycopene to yield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAS07194.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-MAR-2000: 2000EF-0105822
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Best Local Similarity 43.5%; Pred. No. 5.4e-92;
Matches 228; Conservative 94; Mismatches 175;
                                                                                                                                                                                                                                         11 JAN 2000;
                                                                                                                                   (HELI-) HELIX RES INST.
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કેક્કા - પાલુક
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                                                              Isogai T,
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                         Sugiyama T,
                                                                                                                                                                                                        2000 ip-0241899
                                                                                                                                                                                                                                                                                                                                                                                                                 2000EF-0116126
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2000JF-0183767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence SEQ ID NO:12718.
                                                                                                                                                                                                                                                                                                           49 IP-11 (110253
                                                                                                                                                                                                                                                                                                                                            99JP 0248036
                                                          Nishikawa T,
                             Wakamatsu A,
                                                          Hayashi K,
                             Nagai K,
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                                                              Saito K,
                             Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.dels
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                                                              Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GILLERVNYD YNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3' end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 6' end sequence/3' end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the 5602 nucleatide sequences defined in the specification, where the oligonucleatide comprises at least Is nucleatides; or (b) a combination of an oligonucleatide comprising a sequence complementary to the complementary strand of a polynucleatide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynoclectide which comprises and of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                represent oligonucleotides, all of which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   crWAs easily without any specialised methods. AAH08166 to AAH18628 and AAH18633 to AAH18742 represent human cuNA sequences; AAB92446 to AAH18632 AAB96893 represent human amino acid sequences; and AAH13629 to AAH13632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; SEQ ID 12718; 2537pp + CD ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                         264
  474 TCVVVSEPNKAPFILLILDAKTFKELGRATVNVEMHLDLHGMFIP 517
                                                                                                                                                                                                                                                                                    324 QINAFED@GCVIIDLCCQENGRTLEVYQLQNLFKAGEGLDQVHNSAAKSFF -FFFVLFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10
                                                           KKYHEFYGOGER-HIVGDSLIKVDVV-----WPEDGEYPSEPVFVPAPGTNEEDGGVIL 494
                                                                                                                    KKYKYVYATEVOWSPVPTKTAKI.NVOTKEVLHWGEDHOWPSEPTFVPSPDAPEEDEGVVL 473
                                                                                                                                                                      NVSLNAPECDNLSPLSYTSASAVKQADGT:WCSHENLHQEDLEKEGGIEFPQIYYEFFSG
                                                                                                                                                                                                                               QYDKDAEVGSNLVKLP-TSATAVKEKIJGSTYCDPETLA'E-----GTELPKVNYD-YNG 414
                                                                                                                                                                                                                                                                                                                                             HINAYEEDGHVVFCIVAYRDNSLYDMFYLKKLDK+ - DFEVNNKLTSIFTCKFFVVF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FGEYG-ESYKVIRVE---PEKVDLGETIHGVQVICSIASTEKGKPSYYHSEGMIENYIIF 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IVDEGRIKYVLEKIPSSVEEKEKKKSTEKHLEVVOSIESEGLLGESYYHSEGITENYIVE 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YVRYKGDYYLCTETNEMNKVDIETLEKTEKVDWSKFIAVNGATAHPHYDPDGTAYNMGNS 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMKTGDDYYATSETNEIRKIDPQTLETLDKVDYSKYVAVNLATSHPHYDSAGNILNMGTS 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RSKFLQSDTYKANSAKNRIVISEFGTLALPDPOKNVFEPFMSRFELPGKAAAMTDNTNVN 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSKYLPSDTYWONIEANFIVVSEFGTMAYFDECKNIFAKAFS - YLSHILEETUNGLIN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EEAPRG1SARVWGHEPKWLNGSLLK1GPGKFEFGKUKYNHWEUGMALLHGFKMAKGTVTY 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EEHPEPIKAEVQGQLPTWLQGVLLRNGPGMHTIGDTKYNHWFDGLALLHSFTFKNGEVYY 69
                                                                                                                                                                                                                                                                                                                                                                                                   TEQPERMNEMKTATSKT RGKAFSTGT SWERGONT REHVVEKETGET LIEGEVYSKIERVIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                           IEQPEKLDIVKLATAYIRGVNWASCISEHKEUKTWEHEVUEKIKKEVSIKEYILALVLYH 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           539 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85; Mismatches 178; Indels
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SVVITPNQNESNFLLVLDAKNFEELGRAEVPVQMPYGFHGTFIP 538

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AAUU4294
fungi, yeast, insert, animal or plant cells, seeds, rissues, or whole organisms have improved nutritional quality or physiological condition and accountable improved nutritional quality or physiological condition and accountable improved nutritional quality or physiological condition and accountable insputant metabolities of carotene or take up beta-carotene from the medium. Expression systems encoding beta-diox II are useful in the study of beta-diox II activity. Identification of cPNAs encoding beta-diox I and II allows the physiological characterisation of mammalian carotene/retinoid metabolism. Vitamin A production in crops and
                                                                                                                                                                                                                                                              determining the presence or quantity of beta diox II nucleic acid and determining presence and amount of beta diox II. The polypoptide is also useful for increasing on decreasing the amount of beta diox II levels in a cell or tissue which can modify the level of vitamin A and other retinoids. Antibodies are useful for studying beta-diox II localisation,
                                                                                                                                                                                                                                                                                                                                                                                          response studies in relevant models of retiroid/oftamic A deticionary during any stage of an organism's development. The models acids are also useful as probes and as a guideling to define now MCP (polymerase chain reaction) primers for the cloning of substantially homologous DNA sequences from other sources. The nucleic acids are also useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for diagnostic and/or therapeutic purposes and for preparing antisense ribodyme type therapeutic agents and for detecting any abnormality of endogenous beta-diox II. The beta-diox II specific antisense cliponacleutides derived from the ENA sequence are useful for doso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           apolycopenals, respectively. The DNA is useful for transforming grain seeds, c.g. corn; oll seeds, e.g. brassica seeds; edible seeds e.g. palm; bill-b seeds or seeds with ball-b parts - g whick pass potatoes, carrots, sweet potatoes, sugar boots, banana. The polypoptide is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence represents the amino acid sequence of Luman 2, hala carotemedioxygenase (Beta diox II). Beta diox specifically cleaves beta caroteme and lycopene to from beta caroteme and lycopene to from beta caroteme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated mouse, human, zebrafish beta-carotene dioxygenase (beta-diox II) protein that cleaves beta carotene and lycopene to yield beta-apocarotenal and beta-ionone, and apolycopenals, respectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lycopene; beta apocarotenal; beta ionone; apolycopenal; grain seed; corn; oil seed; palm; chick-pea; diagnostic; therapeutic; ribozyme; rethoold/witamin A deficiency; beta-diox II; transgenic; nutrition; carcteme/retinoid pathway; witamin A aldohyde; retinoic acid; crop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAUv4294 standard; Protein; 556 AA
                                                                                                                                                                                                                screening of an expression library to identify modele solds encoding beta-diex II or the structure of functional domains. The transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2, Fig 14, libpp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GREE-) GREENOVATION PELANZENFIOTECHNOLOGIE GMBH
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                                                                                                                                                                                                                                                                      Canine; dog: RPE65, ranine retinal plyment epithelium 65; RPE65; congenital stationary night blindness; CSNB; mutation detection.
             Aquirre GD, Acland GM,
                                                  (CORR ) CORNELL RES FOUND INC
                                                                                         1848 - JUN - 40
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB73955 standard; Protein: 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               microorganisms can be achieved by transforming the organisms or crops
                                                                                                                                                               13-MAR-2001.
                                                                                                                          30-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                       29-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      with the cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   512 SYVITPHQNESNFLLVLDAKNFEELGRAEVPVQMPYGFHGTFIP 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      474 TCVVVSEPNKAPFILIILDAKTFKELGRATVNVEMHLDLHGMFIP 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         453 KKYHFFYGCGFR-HLVGDSLIKVDVVNKTLKVWREDGFYPSEPVFVPAPGTNEEDGGVIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          414 KKYKYVYATEVQWSPVPTKIAKLNVQTKEVLHWGEDHCWPSEPIFVPSPDAREEDEGVVL 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       219 FGPYG-FSYKVIRVP---PEEVDLGETIHGVQVICSIASTEKGKPSYYHSFGMTRNYIIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 QINAFEDGGCVIIDI.CCQDNGRTLEVYQLQNLRKAGFGLDQVHNSAAKSFP--REFVLPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 IVDKGPTKYVLFKIPSSVPEKEKKKSCFKHLEVVCSIPSRSLLQPSYYHSFGITENYIVF 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               159 YVRYKGDYYLCTETNEMNKVDIETLEKTEKVDWSKFIAVNGATAHPHYDPDGTAYNMGNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 IMKTGDDYYATSETNFIRKIDPQTLETLDKVDYSKYVAVNLATSHPHYDSAGNILNMGTS 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 EEHPEPIKAEVÖGÖLFTWIGGVLLKNGFGMHTIGDIKYNHWFDGLALLHSFTFKNGEVYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QYDKDAEVGSNLVKLP-TSATAVKEKDGSIYCQPEILCE-----GIELPRVNYD-YNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HINAYEEDCHVVFDIVAYRDNSLYDMFYLKKLDK-----DFEVNNKLTSIPTCKRFVVPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IEQPLKMNLWKIATSKIRGKAFSDGISWEPQCNTRFHVVEKRTGQLLPGRYYSKPFVTFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IEQPFKLD1VKLATAY1RGVNWASCLSFHKEDKIWFHFVDRKTKKEVSTKFYTDALVLYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSKYLRSDTYNGNIEANRIVVSEEGTMAYPDDCKNIEAKAES--YLSHTIDEETDNCLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NVSLNAPEGDNLSPLSYTSASAVKQADGTICCSHENLHQEDLEKEGGIEFPQIYYDRFSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RSKFLQSDTYKANSAKNRIVISEFGTLALPDPCKNVFERFMSRFELPGKAAAMTDDTNVN 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EEAPRGISARVWGHFPKWLNGSLLRIGPGKFEFGKDKYNHWFDGMALLHQFRMAKGTVTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 556 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                       9805-0103219
                                                                                                                          9908-0385259
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44.1%;
           Ray K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TH 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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RESULT 11 AAR44617

AAR44617;

AAR44617 standard; Protein; 533

Retinol binding protein receptor; retinitis pigmentosa

Human retinol binding protein receptor.

(first cutry)

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Db
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is canine retinal pigment epithelium 65 (RPE65). The gene encoding this protein is useful for identifying dogs which are genetically normal, or are carriers of, or affected with congenital stationary night blindness (CSNB). Carriers for CSNB are identified through the detection of an AAGA deletion at macheolides 487-490 in the canine RPE65 gene. This allows a breeder to eliminate the carrier from the breeding stock or to breed carriers with genetically normal dogs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Fig 1A-1B; 25pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel nucleic acid molecule encoding canine retinal pigment epithelium 65, where presence of mutation in one or both alleles is indicative of a carrier of, or dog affected with rongenital stationary might
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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N-PSDB; AAF79560.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 37.9%; Score 1071; DB 22
Local Similarity 42.2%, Pred. No. 3.1e-88;
  485
                                                471 VVLTCVVVSEPNKAP-FLLILDAKTFKELGRATVNVEMHLDLHGMF 515
                                                                                                                                                                                                                                                                                                        307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190 YNIGNOEGKNESIAYNIVKIF---FLQADKEDFISKSEVVVQFFOSDRFKPSYVHSFOLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 DNALVNYPYGFDYYACTETNFITKINDFTLETTKQVDLCNYVSVNGATAHDHIENDGTV
                                                                                                                                                                                                                                                                                                                                                      301 DALVIYHHINAYEEDGHVVFDIVAYRD-NSLYDMFYLKKIDKDFE---VNNKLISIPICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 DNCLINIMKTGDDYYATSETNFIRKIDPQTLETLDKVPYSKYVAVNLATSHFHYDSAGNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 EKEGEVTYHERFIREDAYVRAMIEKRIVITELGIJAHIDIR KNILSPELSYFROV EVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 FKNGEVYYRSKYLRSDTYNONTEANFTVVSSEFOTMAYFFFFOFNTFAFAFSYLSHTTFEFT TET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 ETV----EELSSPLIAHVIGKTPUNLIGSLUMIGMILEEVISKMEYHLEIMGALLIIKED 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 ETIFNRNKEEHPEPIKAEVQGQLPTWLQGVLLRNGPGMHTIGDTKYNHWFBGLALLHSFT 61
                                                                                                                                                YNGKKYKYVYAIEVQWSPVPIKIAKLNVQTKEVLHWGEDHCWPSEPIFVPSPDAKEEDEG
VVLSVVVSPGAGQKPAYLLILNAKDLSEVARAEVEINIPVTFHGLF 530
                                                                                                                                                                                                        RSVLPLNIDK-ADTGKNLVTLPNTTATATLRSDETIWLEFEVLFSGPRQAFEFFQINYQK
                                                                                                                                                                                                                                                                                                                                                                                                           FNY I VEVETTVK I NIEKTESSWSEWGANYMUETTSNET MGVWEHTAEFAKKAFYENNAYRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENYIVETEQPEKLDIVKLATAY-IMGVNWASGLSEHKEDKTWEHEVDRKTKKEVSTKEYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LNMGTS1VDKGREXVVLEX1FSSVFEXBKKKSGEXHLEVVOS FESKS11.GESYYHSEFFFE
                                                                                                     YGGKPYTYAYGLGLNHF-VPDRLCKLNVKTKETWVWQEPDSYPSEP1FVSHPDALEEDDG
                                                                                                                                                                                                                                                                                                      SSENLEHHINTYEDNEELIVDLCCWKGEEEVYNYLYLANLEENWEEVKKNAFKAFOPEVR
                                                                                                                                                                                                                                                      REVVPLQYDKDAEVGSNLVKLP-TSATAVKEKIGS (YCCPETICEG----) ELLPKVNYD-
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The protein (SEQ. ID NO. 1) may be used to diagnose and tro retinoid linked conditions such as inability to accumulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 15; Page 21-24; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New retinol binding protein receptor and homologue coding nucleic acid molecule - useful for diagnosis and treatment of retinoid linked pathological conditions, for hybridistics in stringent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             retinoids in the eye, leading to retinitis pigmentosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conditions and treating retinitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAQ53070
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les 221; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                          130 DNALVNIYPVGEDYYACTETNFITKVNPETLETIKQVDLCNYVSVNGATAHPHIENDGTV
                                                                                                                                                                                                                                                                                                                                                                                                                                         122 DNCLINIMKTGDDYYATSETNEIRKIDFQTLETLIJKVJYSKYVAVNLATSHEHYUSAGNI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 FKEGHVTYHFRFIRTDAYVRAMTEKFIVITEFGTCAFFDPCKNIFSFFFSYFFGV··EVT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 ETIFNPNKEFHPEFIKAEVQGQLPTWLQGVLLFNGFGMHIIGDTKYNHWFDGLALLHSFT 61
VVLSVVVSPGAGQKPAYLLILNAKDLSEVARAEVEINIPVTFHGLF 530
                                 VVITCVVVSEPNKAP-FILTIDAKTEKELGRATVNVEMHIDLHGMF 515
                                                                                                                                                      SPENIFHHINTYEDHEFLIVDD CWK SFFFVYNYLYLANLRENWEFVKKNAFKAFDEVR
                                                                                                                                                                                                                                    DALVLYHHINAYEEDGHVVEDIVAYRD-NSLYDMEYLKKLDKDEE···VNNKLTSILTCK 356
                                                                                                                                                                                                                                                                       PNY IVFVETPVK INLFKFLSSWSLWGANYMDCFESNETMGVWLHIADKKRKKY INNKYRT
                                                                                                                                                                                                                                                                                                                                                                       LNMGTSIVDKGRTKYVLFKIFSSVPEKEKKKSOFKHLEVVOSIFSFSLIQPSYYHSFGIT 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FKNGEVYYRSKYLRSDTYNCNIEANRIVVSEFGTMAYPDPCKNIFAKAFSYLSHT1PEFT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ETV-----EELSSPLTAHVTGRIPLWLTGSLLROGPGIFEVGSRPFYHI.FDGQALI.HKFP 71
                                                                                                 YNGKKYKYVYATEV@WSPVPTKTAKLNV@TKEVIHWGSCHCWPSEFTFVPSFCAFEEDEG
                                                                                                                                                                                                                                                                                                      ENYIVFIEQPEKLDIVKLATAY-IRGVNWASCLSFHKEDKTWFHFVDRKTKKEVSTKFYT
                                                                   YGGKPYTYAYGLGLNHF-VPDRLCKLNVKTKETWVWQEPDSYPSEPIFVSHPDALEEDDG
                                                                                                                                   RYVERINIOK-ADTOKNEVTERNTTATATE/TSDETEWLEREVLESGREGAREFRGINYOK 425
                                                                                                                                                                                                                                                                                                                                       YNIGNCFGKNFSIAYNIVKIP---PLQADKEDPISKSEIVVQFPCSDRFKPSYVHSFGLT
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42.0%;
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No. 3.9e-88;
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                                                                                                                                                                                                                                                                                                                                                                                                       subjects requiring vitamin A supplementation) and for detecting mutations in the bCDD game. The nucleotide encoding bCOD may also be used to transform cells, particularly plant cells, to increase their vitamin A contents (especially in fruits and vegetables) and it game therefore it subjects who have mutated or deleted forms of the bCOD game and thus low witamin A levels and suspectivity to developmental or ophthalmological disorders. Antibodies raised against bCOD are used for detection/quantification of bCOD in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibodies. Nucleotides encoding all or part of bCOD are useful as primers or probes for specific amplification and/or detection of the gene that encodes bCOD, for isolation of related sequences in other organisms, for determining bCOD lovels in humans (to identify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reta, beta-carotene-15,15'-dioxygenaso (boot) is used for enzymatic conversion of beta-carotene to vitamin A and for raising specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beta,beta-carotene 15,15'-dioxygenase protein, nucleic acids and antibodies, useful for production of vitamin A from carotene and therapy of opthalmological disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beta, beta carotene 15,15 dioxygenase; vitamin A; beta-carotene; transformation; fruit; vegetable; developmental disorder; ophihalmological disorder, antibody, detection, grantification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-FEB-1999;
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                                                                                                                                                                                                                                                                                                     weal Similarity
                                184 MGTSIVDKGRTKYVLFKIPSSVPEKEKKKSCFKHLEVVCSIPSRSLLQPSYYHSFGITEN 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beta-carotene-15,15-dioxygenase
                                                                                                                                          51 TYHRRFIRTDAYVRAMTEKPIVITEFGFTTCAFPDPCKNIFSRFFSYFRGV--EVTDNAL 118
                                                                                                                                                                                                                                                  10 BEHPEP1KAEV@QQQEP1WE@QVCLP++NGPAMBETGOTKYNHWPD31A1LHSETFKNGFV-67
TONOFORNES LAYNIVE LIPPERACKERP KOKETS - BITVVCF FOR BYFKYFKYVHKFCC TEN
                                                                    VNVYPVGEDYYACTETNFITKINPETLETIFTKQVDLCNYVSVNGATAHPHIENDGTVYN 178
                                                                                      YYFSKYLESTIYNCNIEANFIVVSEEG--TMAYPEPCKNIFAKAESYLSHTIPEFTUNCI, 125
                                                                                                                                                                                                              529 AA
                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                  35.9%; Score 42.3%; Pred. No. 4.15 (47.7%) Wismatches 184; Mismatches 184;
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                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and cell-cell interactions in higher eukaryotes for the development of inserticides, therapeutics and pharmaceutical drugs. The invention discluses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                             at ttp.wipo.int/pub/published_pot_sequences
                                              specification, but was obtained in electronic format directly from WIPO
                                                                                   sequences (ABL01840 (ABB57737-ABB72072)
                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 42033, 21pp + Sequence Listing, English
                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid
                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ABL15850.
                                                                                                                                                                                                                                                                                                                                                                                                             Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAR-2000;
11-JUL-2000;
                                                                   The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                    interactions -
                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                               (PEKE ) PE CORP NY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila, developmental biology, cell signalling; insecticide:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster polypophido SEQ ID NO 42033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAR-2002 (first entry)
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                                                                                                                                                                                                                                                                                                   from Drosophila and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 YIVFIEQFEKIDIVKLATAY IRCVNWASCL SFHKEDK-TWEHEVDRKTKKEVSTKEYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   355 CKRFVVPLQYDKDAEVGSNLVKLP-TSATAV--KEKDGSTYCQPEILCEG----IELPRV 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REEDEGVVLTCVVVSEPNKAP-FLLILDAKTFKELGRA--TVNVEMHLDLHGMF 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NYQKYCGKPYTYAYGLGLNHF-VPDRLCKLNVKTKETWFTVWQEPDSYPSEPIFVSHPDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DALVLYHHINAYEEDGHVVFDIVAYRD-NSLYDMF--YLKKLDKDFE---VNNKLTSIPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NYD-YNGKKYKYVYATEVQWSPVPTKIAKLNVQTKEVLH-~WGEDHCWPSEP1FVPSPDA 464
                                                                                                  (AHL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                             Adams M,
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                                                                                                                                                                                                                                                                                                 detection reagent for detecting 1808 or more for elucidating cell signalling and cell-cel
                                                                                                                                                                                                                                                                                                                                                                                                           Myers EW:
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Sequence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                     lycopene; beta-apocarotenal; beta-ionone; apolycopenal; grain seed; oil seed; palm; chick pea, diagnostic, therapeutic, libezyme; retinoid/vitamin A deliciency; beta-dlox II; transgenic; nutrition;
(GREE-) GREENOVATION PELANZENBIOTECHNOLOGIE GMBH
                                        24-bec-1999; 99EP-0125895
20-MAR-2000; 2000EP-0105822
                                                                                                  27-DEC-2000; 2000WO-EP13273
                                                                                                                                             05-JUL-2001.
                                                                                                                                                                                      WO200148153-A2
                                                                                                                                                                                                                             Drosophila melanogaster.
                                                                                                                                                                                                                                                                    carotene/retinoid pathway; vitamin A aldehyde; retinoic acid; crop
                                                                                                                                                                                                                                                                                                                                                   Beta-carotene dioxygenase; beta-diox 1; Drosophila; beta-earotene,
                                                                                                                                                                                                                                                                                                                                                                                          brosophila beta-carotene dioxydenase (beta diox I).
                                                                                                                                                                                                                                                                                                                                                                                                                                 23-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU04291 standard; Protein; 620 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGLNDRYYGLIVLCAKTMTELGRO----DFHTNGPVPKGLHGWFAP 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEPN-KAPFLLILDAKTFKELGRATVNVEMHLD-----LHGMFIP 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YAISSDVDAVNPGTLIKVDVWNKSCLTWCEENVYPSEPIFVPSPDPKSEDDGVILASMVL 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RGRYEEENLVNLVTMEGSQAEAFQGTNG-IQLRPEMLCDWGCETPRIYYERYMGKNYRYF 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VU----SNLVKLPI----SALAVKEKDESTYTQPELLICE-TIELPRVNYF-YNTKYYKYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VEQPLSVSLTEYIKAQLGGQNLSAGLKWFEDKFILFHLIDKVSGKLVOT-YESEAFFYLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IEQPEKLDIVKLATAYIRGVNWASCLSEHKEUKTWEHFVUKKIKKEVSTKFYTDALVLYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MTPSGPAYTIL----SEPHGED---MEEDAHVVATLPCFWKLHPGYMHTPGLTDHYFVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YATEVQWSPV-PTKIAKLNVQTKEVLHWGEDHCWPSEP1FVPSPDAREEDEGVVLJCVVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPEGDQYYTETETPEMHRINPCTLATEAR1CTTDEVGVVNHTSHPHVLPSGTVYNLGTT
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34.6%; Pred. No. 3.2e-67;
valive 99; Mismatches 189; Indels 95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and accumulate important metabolites of caroteme/tetinoid pathways such as vitamin A aldehyde and retinoic acid, beta-carotene or take up beta-carotene from the medium. Expression systems encoding beta-diox II are useful in the study of beta-diox II activity. Identification of cDNAs encoding beta-diox II allows the physiological characterisation of mammalian carotene/tetinoid metabolism. Vitamin A production in crops and microorganisms can be achieved by transforming the organisms or crops
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   determining the presence of quantity of beta diox II nucleic acid and determining presence and amount of beta-diox II. The polypeptide is also useful for increasing or decreasing the amount of beta-diox II levels in a cell or tissue which can modify the level of vitamin A and other retinoids. Antibodies are useful for studying beta-diox II localisation, screening of an expression library to identify nucleic acids encoding beta-diox II or the structure of functional domains. The transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      carrots, sweet potatoes, sugar beets, banana. The polypeptide is useful for diagnostic and/or therapeutic purposes and for preparing antisense or ribozyme type therapeutic agents and for detecting any abnormality of endogenous beta-diox II. The beta-diox II specific antisense oligonucleotides derived from the DNA sequence are useful for dose response studies in relevant models of retinoid vitamin A deficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              during any stage of an organism's development. The nucleic acids are als useful as probes and as a guideline to define new PCR (polymerase chain reaction) primers for the cloning of substantially homologous DNA sequences from other sources. The nucleic acids are also useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fungi, yeast, insect, animal or plant cells, seeds, tissues, or whole organisms have improved nutritional quality or physiological condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seeds, e.g. corn; oil seeds, e.g. Brassica seeds; edible seeds e.g. palm edible seeds or seeds with edible parts e.g. chick-peas; potatoes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated mouse, human, zebrafish beta-carotene dioxygenase (beta-diox II) protein that cleaves beta carotene and lycopene to yield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              with the cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          apolycopenals, respectively. The DNA is useful for transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 carotene and lycopene to form beta-apocarotenal and beta-ionone, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence represents the amino acid sequence of Drosophila beta-carotene dioxygenase (Beta-diox I). Beta-diox specifically cleaves beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 6; 116pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local similarity
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308 HINAYEEDGHVVFDIVAYRDNSIYDMFYLKKLDKDFEVNNKLTSIPTCK--PFVVPL---
                                                                                                     248 IEQPEKLDIVKLATAYIRGVNWASCLSFHKEDKTWFHFVDRKTKKEVSTKFYTDALVLYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                     VEQPLSVSLTEYIKAQLGGQNLSACLKWFEURFILFHLIDRVSGKLVQ1-YESEAFFYLH 337
                                                                                                                                                                   MTPSGPAYTIL.
                                                                                                                                                                                                                IVDKGRTKYVLEKIPSSVPEKEKKKSCFKHLEVVCSIPSRSLLQPSYYHSEGITENYIVE 247
                                                                                                                                                                                                                                                                                                                                                                               YQNREVDTETLRKNRSAQRIVVTEFGTAAVPDPCHSIFDR---FAAIFRPDSGTDNSMIS
                                                                                                                                                                                                                                                                                                                                                                                                                               YRSKYLRSDTYNCNIEANRIVVSEFGTMAYPDPCKNIFAKAFSYLSHTIPEF-TDNCLIN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEEHPEPIKAEVQGQLPTWLQGVLLRNGFGMHTIGDTKYNHWFDGLALLHSFTFKNGEVY 68
                                                                                                                                                                                                                                                                      TYPEGDOYYTETETPEMHPINPOTLATEAPIOTOFVGVVNHTSHPHVLPSGTVYNLGTT
                                                                                                                                                                                                                                                                                                                      IMKTGDDYYATSETNEIRKIDPQTLETLDKVDYSKYVAVNLATSHEHYDSAGNILNMGTS 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        620 AA;
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34.5%;
                                                                                                                                                              --SEPHGEQ---MEEDAHVVATLPGFWELHFGYMHIEGLIDHYEVI 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99; Mismatches 189; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 840.5; DB 22; Pred. No 3.2e-67;
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                                                               are useful in the study of beta-diox activity, Identification of cDNAs enveloped beta-diox allows the physiological characterization of mammalian vitamin A metabolism. Vitamin A production in crops and
                                                                                                                                                                                                                                                                                                   Dioxygenase (beta-diox) protein that cleaves beta carotene to form vitamin A aldehyde, and polynucleotides encoding them useful for producing transgenic bacteria, fungi, plants expressing the polypep
Sequence
                                                    microorganisms can be achieved by transforming the organisms or crops
                                                                                                                      up beta-carotene from the medium. Expression systems encoding beta-diox
                                                                                                                                       plants. The transpense plants have improved outritional graphs tological condition and accumulate vitamin A aldebydo
                                                                                                                                                                          polypeptide. Beta-diox specifically cleaves beta-carotene to form vitamin A aldehyde. Beta-diox is is useful for producing transgenic
                                                                                                                                                                                                                                                  Claim 7; Fig 6, 87pp, English.
                                                                                                                                                                                                                                                                                                                                                                            WFI, 2001-441713/47.
N-FSDB; AAH42156.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beta-carotene dioxygenase; beta-diox; beta-carotene; vitamin A aldehyde;
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                                                                                                                                                                                                              The present sequence represents a beta-carotene dioxygenase (beta-diox)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        576 GGINDRYVGLIVICAKTMTELGRO----DFHTNGPVPKOLHGWFAP 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lubu; LubucEt alocal2
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                                                                                               516 YAKSSDVDAVNPGTLIKVDVWNKSCLTWCEENVVPSEPIFVPSPDPKSEDDGVILASMVI, 575
576 GGLNDRYVGLIVLCAKIMTELGRC----DFHTNGPVPKCLHGWFAP 617
                                                 479 SEPN-KAPFILIIDAKTFKELGRATVNVEMHLD-----LHGMFIP 517
                                                                                                                                                   420 YATEVQWSPV-PTKIAKLNVQTKEVLHWGEDHCWPSEPIFVPSPDAREEDEGVVLTCVVV 478
                                                                                                                                                                                                  457 KÖRYEEENLYNLYTMEGSQAEAFQGING-IQLKPEMLCDWGCETPRIYYERYMGKNYRYF 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       227 MTKSGPAYTII.----SPPHGEQ---MFEDAHVVATLPCKWKLHPGYMHTEGLTDHYFVI 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167 IYPFGDQYYTFTETPFMHRINPCTLATEAPICTTDEVGVVNHTSHPHVLPSGTVYNLGTT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 YONKEVDTETLRKNRSAGRIVVTEFGTAAVPDPCHSIEDR---FAAIFRPDSGTDNSMIS 166
                                                                                                                                                                                                                                                      370 VG----SNLVKLPT----SATAVKEKDGSIYCQPEILCE-GIELPRVNYD-YNGKKYKYV 419
                                                                                                                                                                                                                                                                                                                                                                                                               338 IINCFERDGHVVVDICSYRNPEMINCMYLEAI-ANMQTNPNYATLERGRPLREVLPLCTI 396
                                                                                                                                                                                                                                                                                                                                                                                                                                             408 HINAYEEDGHVVFDIVAYRDNSLYDMFYLKKLDKDEEVNNKLTSIPTCK---REVVPL--- 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 279 VEOPLSVSLTEYIKAOLGGONLSACLKWFEDRPTLFHLIDRVSGKLVQT-YESEAFFYLH 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248 LEOPFKLDIVKLATAYIRGVNWASCLSFHKEDKTWFHFVDRKTKKEVSTKFYTDALVLYH 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188 IVDKGRTKYVLFKIPSSVPEKEKKKSCFKHLEVVCSIPSRSLLQPSYYHSFGITENYIVF 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 IMKTGDDYYATSETNFIRKIDPQTLETLDKVDYSKYVAVNLATSHPHYDSAGNILNMGTS 187
                                                                                                                                                                                                                                                                                                          397 PPASTAKRGLVKSESLAGLSAPQVSKTMNHSVSQYADTIYMPTNGKQATAGEESPKRDAK 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 EREIVDPIEGHHSGHIPKWICGSLLRNGPGSWKVGDMTFGHLFDCSALLHRFAIRNGRVT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 KEEHPEPIKAEVQGQLPTWLQGVLLRNGPGMHTIGDTKYNHWFDGLALLHSFTFKNGEVY 68
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Search completed: July 15, 2003, 09:27:36 Job time: 75 secs

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Genfore version 5 1 6
Copyright (c) 1993 - 2003 Compugen Ltd

OM protein - protein search, using sw model

Run on: July 15, 2003, 09:24:29 , Search time 43 Seconds (without alignments) 1175.970 Million cell updates/sec Title: US-10-063-192-1 175.970 Million cell updates/sec Sequence: METIFNENKEEHPEPIKAEV . MHIGHEMFIFQNEUGAETE 526

Scoring table: BLOSHM62 Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 95134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 20000000000
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Pred. Not is the number of results predicted by change to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Database ·

PIR_73.*
1: pirl:*
2: pir2:*
3: pir3:*
4. pir4.*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SUMMARIES

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A; Status: preliminary
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A:Note: published_errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an
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460 KSETLPGIVKANLENGDHKVWPPENDKQIG--GEPIFVPNPEGVKEDUGILIVPVMTISU 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 GLYACTETPNMHRVDLDSLDTI EPVDFSKYVALHTCTAHQLFDENGDVYNIGSRFGPDAA 222
                                                                                                                                                                                                                                                                                                                      341 RDGCLVVDYCRIEQAGNFDALLIENM-KTGNFQNDALFLPYLTRVIIPLS1PDGAQFGDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223 HVFTVTKNPKNL-QSDSDRS-WEHTTKIGEIRCSETFYPTYMHSFGMSENYLIMFESPIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 DYYATSETNFIRKIDPQTLETLDKVDYSKYVAVNLATSHPHYDSAGNILNMGTSIVDKGR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   471 VVLTCVVVSEPNKAP-FLLILDAKTFKELGRATVNVEMHLDLHGMF 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        411 YNGKKYKYVYATEVQWSPVPTKIAKLNVQTKEVLHWGEDHCWPSEPIFVPSPDAREFDEG 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      367 RYVLPLNIDK-ADTGKNLVTLPNTTATAILCSDETIWLEPEVLFSGPRQAFEFPQINYQK 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 LRSDTYNCNIEANRIVVSEFGTMAYPDPCKNIFAKAFSYLSHTIPEFTDNCLINIMKTGD 133
                                                                              WSPVPTKIAKLNVQTKEVLHWGEDH----CWPSEPIFVPSPDAREEDEGVVLTCVVVSEP
                                                                                                                                                             LLKPLGWAKGCSAIFQDDGKIRLKEKPVCDISMEFPRYHWEKINMKPYNYVYGSSVLGAQ
                                                                                                                                                                                                                                   LVK---LPTSATAVKEKDGSTYCQPEILCE-GIELPRVNYD-YNGKKYKYVYATEV---Q
                                                                                                                                                                                                                                                                                                                                                                                                     EDGHVVFUIVAYRDNSLYDMFYLKKLDKDFEVNNKLTSIPTCKRFVVPLQYDKDAEVGSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDIVKLATAYIRGVNWASCLSFHKEDKTWFHFVDRKTKKEVSTKFYTDALVLYHHINAYE 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TKYVLFKIPSSVPEKEKKKSCFKHLEVVCSIPSRSLLQPSYYHSFGITENYIVFIEQPFK 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LESENYKKNMEAQRIVTGSFGTASFPDPCKSIFSRFFSSFVQS-EGIHDNANVAFAPVGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPIKAEVOGQLPTWLQGVLLRNGPGMHTIGDTKYNHWFDGLALLHSFTFKNGEVYYRSKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPKLCSTSGSVPSYLKGTMLKNGPGMFEIGDTKYGHWFUGMGFIQKYHFEDGKMYYSARY 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YGGKPYTYAYGLGLNHF-VPDRLCKLNVKTKETWVWQEPDSYPSEPIFVSHPDALEEDDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.6%; Score 778.5; DB 2;
31.7%; Pred No. 1.2e-47;
vative 110; Mismatches 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 556;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 280
                                                                                                                                                                                                  RESULT 4
S76169
                hypothetical protein - Symechocystis sp. (strain PCC 6803)
C:Species: Symechocystis sp.
A;Variety: PCC 6803
C:Enter 25-April 27 seepsemb_levision of April 27 at all distance the continues of th
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C; Accession: S76169
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hyporhetical protein T16118 20 - Arabidopsis thaliana (Species, Arabidopsis thaliana (Species, Arabidopsis thaliana (Mouse ear cress) C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999 C:Accession: T10688 R;Beyan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandreum, M.A.; Harrell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A/Cross references EMBL AL049915, GSPNB GN00062, ATSP T16118.20 A/Experimental source: cultivar Columbia; BAC clone T16118 C/Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajan
submitted to the Protein Sequence Database, June 1999
A;Reference number: Z16533
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A, Residues: 1 616 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Introns: 105/3; 359/3; 425/2; 549/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: ATSF:T16118.20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                  447 GEDHCWPSEP1FVPSPDAREEDEG 470
                                                                                                                                                                                                                        414 KKYKYVYATEVQW---
                                                                                                                                                                                                                                                                                                  425 FIGRERIPLD------GSKYGKLEIAVEA--EKHG------KAMDMCSINPLYLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213 GRVMCLTET----QKGSILVDHETLETIGKFEYDDVLSDHMIQSAHFIVTET----EMWTL 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 V@GQLPTWL@GVLLKNGPGMHTTGDTKYNHWFDSTALLHSFTFKNGEVYYRSKYTRSDTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIEQPFKLDIVKLATAY---IRGVNWASCLSFHKEDKTWFHFVDRKTKKEVSTKFYTDAL 303
HEHGMIPSEPFFVPRPGATHEDDS
                                                                                                                                             _CKYKYYYAGGAGERGNEFNALKKYTYTEGTTGFGYVTYINEFFGNGMYGYTTYEFKXYKNX
                                                                                                                                                                                                                                                                                                                                                                         K--REVVPLQYDKDAEVGSNLVKLPTSATAVKEKDGSIYCQPEILCEGIELPRVNYDYNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                VTFHFINAYEEDKNGUGKATVIIADCCEHNADTRILDMLRLDTL----RSSHGHDVLFDA 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLYHHINAYEEDGH------VVFDIVAYR-DNSLYDMFYLKKLDKDFEVNNKLTSIPTC 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TVDKGRTKYVLEKTPSSVPEKEKKKSCEKHLEVVCSTPSBS-11.QPSYYHSEGTTENYTV-246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D-YYATSETNEIRK----IDEQTLETLUKVUYSKYVAVNLATS-HEHYDSAGNILNMGIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPEMPLKYSVKNLLKAEPIPLYKFEWC-----PQDGAFIHVMSKIFF-GEVVASVEVPAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPDEVKPGYRVVRMEAGSNKF------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15,5%;
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                                                                                                                                                                                                                        ----SPVPTKIAKLNVQTKEVLHW 446
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R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima